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; Search time 4314.97 Seconds (without alignments) 11614.233 Million cell updates/sec
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Pred. No.

AK281580 Sequence AC005941 Homo sapi AC005971 Homo sapi AX289502 Sequence AX099802 Sequence AX099802 Sequence AX09803 Sequence AX095774 Sequence AX095774 Sequence AX095774 Sequence AX095774 Sequence AX095774 Sequence AX095774 Sequence AX095773 Sequence AX099773 Sequence AX099773 Sequence AX099774 Sequence AX099774 Sequence AX099803 Sequence AX198131 Sequence AX19813 Sequence AX19813 Rattus no AC12502 Human BNA AC002111 Homo sapi AC002111 Homo sapi AC12847 Rattus no AC019111 Mus muscu AC101988 Human PAC AC101117 Mus muscu AC101111 Mus muscu PAT 03-NOV-2001 Andersson,L., Luthman,H. and Marklund,S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 3 18-OCT-2001; Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. linear DNA SUMMARIES ALIGNMENTS Sequence 3 from Patent W00177305. RNU42413 RATNESTIN AC129422 AB046627 AC007111 AC007111 AC097269 AC012171 AC12171 AC126352 AC026353 AC126955 AX281580.1 GI:16608831 222 DB 97.0 152129 97.0 152129 9.8 206854 9.8 2109 9.8 2115 9.8 2115 9.8 2115 2.2 1867 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.2 1873 2.1 1873 2.2 1873 2.2 1873 2.1 1873 2.2 1873 2.2 1873 2.1 1873 2.2 1873 2.1 1873 2.2 1873 2.2 1873 2.3 1873 2.4 1873 2.7 1873 2.8 1873 2.9 1873 2.1 1873 2.1 1873 2.1 1873 2.2 1873 2.3 1873 2.4 1873 2.7 1873 2.7 1873 2.8 1873 2.9 1873 2.1 1873 2.1 1873 2.1 1873 2.2 1873 2.3 1873 2.4 1873 2.7 1873 2.8 1873 2.9 1873 2.1 1873 Length 82806 192180 196413 198172 239434 74645 138312 238325 41680 58725 63680 78215 184288 Ouery Match human. RESULT 1
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AC027416/c
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LOCUS
BDEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152129)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-504G11

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113191 123496: contig of 10306 bp in length
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21928: contig of 2362 bp in length
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38179: contig of 4111 bp in length
38279: gap of 100 bp
42366: contig of 4087 bp in length
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73218: contig of 6523 bp in length
73318: gap of 100 bp
77115: contig of 3797 bp in length
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhalalter, B., Brown, A., Burkett, G., Campopiano, A., Cascle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cascle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cascle, A., Choepel, Y., Colangelo, M., Collins, S., Codgran, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karnino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand-Pierre, N., Grant, G., Line, S., Goyette, M., Graham, L., Klein, J., LaRocque, K., Lamazares, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Landzers, R., Macdonald, P., Marquis, N., McCarthy, M., McEban, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisanic, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Schauer, S., Severy, P., Spencer, B., Scanger-Thomann, N., Schauer, S., Severy, P., Spencer, B., Santos, R., Schauer, S., Severy, P., Spencer, B., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassillev, H., Viel, R., Vo, M., Wille, M., X., Wyman, D., Ye, W.J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using Repeatmasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 504 G 11

Sequencing vector: M13 M77812 100% of reads
Sequencing vector: M13 M77812 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 145376 bases at least Q30
Consensus quality: 145264 bases at least Q30
Consensus quality: 146503 bases at least Q30
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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------ Project Information
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2403 2502: gap of 100 bp
2503 3823: contig of 1321 bp in length
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3924 5020: contig of 109 bp in length
5021 5120: gap of 100 bp
5121 6161: contig of 1041 bp in length
6162 6261: gap of 100 bp
6262 7547: contig of 1286 bp in length
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15043: contig of 2387 bp in length
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	35899 35899 780 35838	35778 901 35718 961 35658	1080 1080 1140 1140 1200	CTCCCTAGGCTGCCCCGAGGCTCACTGCTGCTGCTGCTGCTGCTGCTGTTTGAAGCTGTCTA 1260	1440 3517 1500 3511
/note="assembly_fragment clone_end:SP6 misc_feature 1956721928 misc_feature 22029. :24319 misc_feature 7.0029. :24319 misc_feature 7.0029. :24319 misc_feature 7.0029. :24319 misc_feature 7.002e="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" misc_feature 7.002e="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment" /note="assembly_fragment"	misc_feature 3828043366 misc_feature 42467 .46386 misc_feature 42467 .51285 misc_feature 51286 .51285 misc_feature 51386 .55871 misc_feature 55872 .60595 misc_feature 60696 .66595	misc_feature 6696.73218 misc_feature 7319.77115 misc_feature 7319.77115 misc_feature 7216.383embly_fragment" misc_feature 85123.33114 misc_feature 85123.33114 misc_feature 93415.101193 misc_feature 701294.11393 misc_feature 701294.11393 misc_feature 701294.113991	DB 2; Length 152129; s 1; Indels 0; Gaps GGGCCAACGGTGGGGGGCG 60	121 GGAGATGGAGGGGGAGATCTTGTGGGTGGGGGGGGGGGG	36318 ATGACCAGGAGACCTTTCACCTCGTTACTGCTGGCCTGGCCTGGGCGTGGTGGTGTGGTGGTGGTGG

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FEATURES
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dicine, 4444 Forest Park Parkway, St. Louis,
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 206854) Sulston,J.E. and Waterston,R.
Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MOG 3108, USA (bases 1 to 206854)
                                                                                                                                                                                                                                                                                        AC009974 206854 bp DNA linear PRI 09-JJ
Homo sapiens BAC clone RP11-459119 from 2, complete sequence
AC009974
                                                      TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                                                                                                      CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA
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Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
Upublished (2001)
3 (bases 1 to 206854)
Waterston,R.H.
                                                                                                                                                                                            1681 CGAATGTGGTACCCACCCCAGGATGAGAGGCTCGGGCTGG 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson;wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University School of Medicine,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                  AC009974.9 GI:16799058
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Waterston, R.H.
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Homo sapiens
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J., J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: BBACG3.6
NEIGHBORING SEQUENCE INFORMATION:
                    all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NID:98364652) tz39c01.y1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Data from AC079810 and AC073128 was used to finish this clone,
     otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RPI1-1077K22; the clone sequenced to the right is RPI1-64705. Actual start of this is at base position 1 of RPI1-459I19; actual end is at base position 206854 of RPI1-459I19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF183086 (NID:911061273) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NID:98042860)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST C05773 (NID:g1502549)"
This sequence was finished as follows unless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .37
/note="match to EST AW880850
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'note="match to EST BE314060
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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'note="match to EST
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note="match to EST
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/note="match to EST A1670836 (NID:g4850567) wa04g10.x1"

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center project name: H_NH0459119

281344 //note="match to EST AL567345 (NID:g12920610)"	201374 Potce - match to EST AW880850 (NID:g8042860)" 28]344	e="match to EST BE047599 (NID:g8364652) tz39c01.y1"		e="match to EST BE908408 (NID:g10402954)" .344	/note="match to EST BF183086 (NID:g11061273)" 281 344	/note="match to EST BF304755 (NID:g11251653)" 281, 344	/note="match to EST BG477625 (NID:g13409904)" 281. 344	/note="match to EST BI059713 (NID:g14467240)"	/note="similar to Homo sapiens EST BI114348 (NID:914565249)"	o ES	α· ω·	588929 //note="match to EST T64073 (NID:g667938) yc05d12.rl" 6.a.	note="04" Note="match to EST BI059713 (NID:g14467240)" 94 - 763		73 753 note="match to EST A1670836 (NID:94850567) wa04910.x1" 94 763	a)	a)	.763 =="match to EST BF183086 (NID		/note="match to EST BG470047 (NID:g13402322)"		/note="10" similar to Homo sapiens EST BI114348 (NID:ca14565240)"		/note="match to EST BE047599 (NID:g8364652) t239c01.y1" 594731	/note="match to EST BE314060 (NID:g9134719)" 599763	/note="match to EST AL567345 (NID:g12920610)" 6171084	/note="match to EST AA481361 (NID:92210913) zv44e01.rl" 622 763	/note="match to EST AI860958 (NID:g5514574) w1S6f05.x1" 622. 763	note="similar to Mus musculus EST AI196847 (NID:g3749453)	564. 763 /note="match to EST BG992568 (NID:014396638)"	CONTRACTOR OF BUILDING CONTRACTOR OF THE PROPERTY OF THE PROPE	TX: SOUTHERN (TEACH) FROM THE CONTRACT OF THE	EST AA043371 (NID:g1521226	/note="similar to Homo sapiens EST BI114348 (NID:g14565249)" 9671085
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Length 206854;

DB 9;

85.9%; Score 1479;

Query Match

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                                                Db 166697 CCTGGCCCCTCAGATCAAGAGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGGAGC 166638
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                                                                             CCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGGAGAGGCTGGGGAGGGTGAAG
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                                                                                                                                                                                                                                                           301 ATGACCAGCTGACCTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG
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    Pred. No. 0;
0; Mismatches
Best Local Similarity 99.9%;
Matches 1719; Conservative
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165679 CTCCATCTCTCTAATGATAGGTGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCTCCT 165620
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Db 165619 ACAGTCCCCTTCCCCAGTCCCACTCAGACCTCCTCAGGCGGCACA 165560
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        CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTCTCTGCACTGCCTGTGGTCA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         165439 CACCTCATCAAGAACGGATCCATCGCCTGCTGTTTTGACCCGGTGTCAGGCAACGT
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                                                                                                                                                                                                         1261 CACCCTCATCAAGAACCGGATCCATCGCCTGTTTCTTGACCCGGTGTCAGGCAACGT
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Sequence 5 from Patent WO0177305.
AX281582 AX281582.1 GI:16608833
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DPAGYGFPPTGMDCLESDCTAGAAGSSTDDVELATEPPATEMECELEGGLLEERPALC
LUSPQAFPRICKGWDDELKRPGAQIYMERMQBHTCYDAMATSSKLVI FDTWLEIKKAFFA
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VGLYSFFDVIHLAAQQTVHNLDMSVGBALRQRFLCLEGVLSCQPHESIGEVIDRIARE
QVHRLVLUVDETQHLGAVSLSDILQALVLSPAGIDALGA"

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YRTIQDLGGTGFRDLAVLETRPILTHALDIFVDRRVSALPVNNECGQVVGLVSRFPDVI
YRTIQDLGGTGFRDLAVLETRPILTHALDIFVDRRVSALPVNNECGQVVGLVSRFPDVI
YRAAQQTYNHLDMSVGEALRQFILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE
TQHLLGVVSLBDILQALVLSFAGIDALGA"

621 c 560 g 470 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mawmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2109)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and Chardon, P.
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Parent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ern
Location/Qualifiers

1. 2109
/organism="Homo Sapiens"
/db_xref="taxon:9666"
/72_.1389
/note="unnamed protein product"
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100.0%; Pred. No. 2.6e-78;
iive 0; Mismatches 0;
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9.8%; Score 168; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 2.5e-78;
Matches 168; Conservative 0; Mismatches 0;
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Sequence 3 from Patent WO0120003.
AX099776 GI:13538810
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us-09-826-581-3.oligo.rge

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

CDS

DEFINITION

RESULT 6 AX099802 LOCUS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 711).
Milan, D., Jeon, 7.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. A. mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trainities on = "MORTEGENSSSWPSPAVTSSSERIRGKRRAKALRWTROKSVEEG EPPGGGEGPRSRPARESTGLEATFRYTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG STOVELATEFPATEMECELEGILEERPALCISPQAPFRIGWDDELKRPGAQIYM RFWGEHTSTVANGVEAPLWDSKKQSFVGMLTITDFILVLHRYTRSPLVQIYELEGHK.EFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYTRSPLVQIYELEGHK.ETWREIYLQGCFKPLVSISPNDSLFEANYTLIKNRIHRLPVLDPVSGNVLHILTHKRLIKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLGAVLETALDIFVLDPVSGNVLHILTHKRLIKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDLGAVLTLUTALDIFVLDFVSGNVLHCKHIFGSLLPRPSFLYRTIQDLGIGTFRDLGAVLTLUTALGLGGVGAVSLSPROTANTIQDKSVNHLDMSV GEALAQRTLCLGGVGAVSGQPHESLGGVIDRIARREQVHRLVLVDBTQHLLGVVSLSDILLQALVSPAGIDALGA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1583 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATC 1642
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/protein_id="AAF73987.1"
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1. .2115
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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1. .1395
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                                      GI:8215681
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/ db_xref=
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                    1583 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATC 1642
                                                                 the
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Patent: WO 1220003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
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Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
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100.0%; Pred. No. 2.5e-78;
tive 0; Mismatches 0; Indels C
                                                                                                                                                     TTGTGGACCGGCGTGTGTCTCCACTGCCTGTGGTCAACGAATGTGGT 1690
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/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Sequence 29 from Patent WO0120003.
AX099802
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1395
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Matches 168; Conservative
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Gaps

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Query Match

928

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988

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1643 1048

BASE COUNT ORIGIN

1047

PRI 07-APR-2000

linear

đq 2290

HSA249977

DEFINITION

AF214519 RESULT 7

AUTHORS TITLE

REFERENCE

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL

FEATURES

AUTHORS

gene

CDS

PUBMED REFERENCE

MEDLINE JOURNAL

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AF336381 227724 bp DNA linear HTG 02-APR-2001
Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN
PROCRESS ***, 3 unordered pieces.
                                                                  Homo sapiens
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                      The (bases 1 to 106)

Robic, A., Jeon, J.-T., Rey, V., Amarger, V., Chardon, P., Looft, C., Andersson, L., Gellin, J. and Milan, D.

Construction of a high-resolution RH map of human 2q35 region on TNG panel and comparison with physical map of porcine homologous Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1622 ATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTC 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primers were defined on sequence AA178898 (cDNA). No intron.
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                                                                                                                                                                                                                                                                                                                                                    Genetique Cellulaire
Institut National de Recherche agronomique (INRA)
BP27, 31326 Castanet Tolosan, France
Tel: (33) 5 61 28 51 21
Fax: (33) 5 61 28 53 08
Email: arobic@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial incubation: 94 degrees C for 4 min
Denaturation: 94 degrees C for 30 seconds
Annealing: 55 degrees C for 30 seconds
Polymerization: 72 degrees C for 30 seconds
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2e-18;
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Tag Polymerase: 0.1 units/reaction
Total Vol: 15 ul
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone lib="Human"
1. .>106
1. .18
                                                                                                                                                                                                                                                                                                                                   Contact: Annie ROBIC, Denis MILAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR cycles: 33
Thermal cycler: Perkin Elmer 9600
Protocol:
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: TGGGCATCGGCACATTCC
Primer B: GACCACAGGCAGTGCAGCA
PCR Profile:
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Primer: each 0.5 uM
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HTG; HTGS PHASE1.
Mus musculus.
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MgCl2: 2 mM
KCl: 50 mM
Tris-HCL: 20 mM
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Matches 57; Conservative
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AF336381/c
                                                                                                                                       REFERENCE
AUTHORS
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/product="Amp-activated protein kinase gamma 3 subunit"
/product="Amp-activated protein kinase gamma 3 subunit"
/product="Amp-activated protein kinase gamma 3 subunit"
/db_xref="G1:66882117.1"
/db_xref="G1:66882117.1"
/db_xref="G1:66882117.1"
/db_xref="G1:66882117.1"
/db_xref="MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAVTS
SSERINGKRARALEMTROKSVEEGEPPGGGEPRSRPAABSTGLEATFPKTTPLAQA
DPAGVGTPPTROKCLSPGTRAAGSSTDDVELATEPPATEARRECLEELERRPALC
LSPQAPEPKLGMSPDELRREGANYTHTREITCYDAMATSSKLVIFDTMLETKRAFFA
LVANGVRAAPLWDSKKOSFVGMLTTDFILVLRRYYRSPLOITFBEGHKTETRREITY
LOGGCFRELVSISPNDSLFEANYTLIKNRIHRLDVLDPVSGNVLHILTHKRLLKFELHIF
GSLLEPRPSFLXTTODLGIGTFRDLAVVLETAPILTALDIFUDRRVSALPPVNNECGOV
VGLYSRFDVIHLAAQOTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDBTOHLLGVVSLSDILQALVLSPAGIDPSGGPEKI"

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Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
AJ249977
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1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
                                                                                                                                AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM

Location/Qualifiers
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A898 Human Homo sapiens STS genomic, sequence tagged site.
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/db_xref="taxon:9606"
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STS.
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Direct Submission
                                                                                                                                                      Homo sapiens.
Homo sapiens
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LWDSKKQSFVCMLTITDFILVLHRYYRSPLVQIYEIEBHKIEFWREIYLOGCFKRLVS
ISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla, Suina, Suidae, Sus. 1 (1885) L. 1987).
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                              Direct Submission
Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular
Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
NOTE: This is a "working draft" sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
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100.0%; Pred. No. 1.3e-09;
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    1 (bases 1 to 227724)
Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A.
Mouse chromosome 1 genomic sequence
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/db_xref="taxon:9823"
472. 1389
/note="unnamed protein product"
/codon_start=1
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2.3%; Scote 5, 25
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 39; Conservative 0; Mismatches
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/organism="Mus musculus"
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Sus scrofa
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REFERENCE
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TQHLLGVVSLSDILQALVLSPAGIDALGA"
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Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Galllard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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100.0%; Pred. No. 1.5e-08;
ive 0; Mismatches 0;
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1. .1873
/gene="PRKAG3"
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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Best Local Similarity 100.0
Matches 38; Conservative
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2.2%; Score 38; DB 4; Length 1873;

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/db
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/brotein id="CAD32626.1"
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/db_xref="GL1109"
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HFWQEHTCYDAMATSSKLVIFDTHMEIKKAFFALVNAGCRRAPLSHDSKGGSFGGMLTI
TDFILVLHRYYRSPLVQITSIEHKIIETWRBIYLGGCFKPLVSISPNDSLFEAVYALI
KNRIHRLPVLDPVSGAVLHILTHKRALLKFLHIFGGLYGCFKPLVSISPNDSLGTFRDL
AVVLETAPTLTADIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRGRATLCLGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGAVSLSDILQ
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 3 14 MAR-2002;
Iowa State University Research Foundation, Inc. (US)
             Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
Location/Qualifiers
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100.0%; Pred. No. 1.5e-08;
iive 0; Mismatches 0;
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Local Similarity 100.0%; Pred. No. 1.5e-08;
tes 38; Conservative 0; Mismatches 0;
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AX398333
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                                                                                                                                              /db_xref="taxon:9823"
1. .1395
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                                                                                          1. .1873
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G. Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
                                      Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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tive 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-08
tive 0; Mismatches 0
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AX099800
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AX398331 GI:21261106
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1. _1395
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OY 1562 ATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGC 1599

DD 967 ATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGC 1004

Search completed: January 7, 2003, 20:11:10 Job time : 4937.97 secs

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January 6, 2003, 17:17:03 ; Search time 479.092 Seconds (without alignments) 1486.844 Million cell updates/sec
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Database :

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Pto7_NBW PUBLseq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 10, Appli Sequence 1402, Ap Sequence 2, Appli Sequence 2, Appli Sequence 22801, Appli Sequence 22801, Appli Sequence 6044, Ap Sequence 6044, Ap Sequence 230, Appli Sequence 6044, Ap Sequence 1075, Appli Description US-09-826-581-5 US-09-826-581-3 US-09-826-581-3 US-09-826-581-3 US-09-826-581-3 US-09-84-761-3173 US-09-84-761-2146 US-09-974-700-1402 US-09-974-700-1402 US-09-974-300-1402 US-09-935-720-2 US-09-864-761-22801 US-09-960-352-2438 US-09-964-761-668 US-09-962-436-230 US-09-982-107-1075 US-09-925-300-665 US-09-925-300-665 US-09-919-497-18 US-09-967-768A-303 SUMMARIES 1100 1100 1100 1100 1100 В Query Match Length Score 1647 278 168 168 52 52 20 19 19 18 18 18 18 18 18 Result Š.

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181 GGCCAAAGCCTTGAGATGGACAAGGCAGAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCA 240

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61 CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAATGAGCTTCCTAGAGCAAAAACAG 120

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CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAAACAG

10 US-09-764-847-1315 Sequence 1315, Ap 10 US-09-764-847-1313 Sequence 1313, Ap 10 US-09-803-661-3 Sequence 3, Appl 10 US-09-938-842A-642 Sequence 642, Appl 10 US-09-938-842A-642 Sequence 642, Appl 10 US-09-834-975-685 Sequence 1685, Appl 10 US-09-834-975-685 Sequence 1431, Appl 10 US-09-934-456-1746 Sequence 1431, Appl 10 US-09-974-456-1746 Sequence 1746, Appl 10 US-09-9738-626-1429 Sequence 1429, Appl 10 US-09-867-701-3768 Sequence 1429, Appl 10 US-09-984-701-3768 Sequence 1429, Appl 10 US-09-984-711-3768 Sequence 794, Appl 10 US-09-920-300A-1146 Sequence 794, Appl 10 US-09-920-300A-1146 Sequence 1146, Appl 10 US-09-928-1146 Sequence 1146, Appl 10 US-09-998-598-904 Sequence 139, Appl 10 US-09-984-153 Sequence 139, Appl 10 US-09-98-598-904 Sequence 139, Appl 10 US-09-98-598-904 Sequence 139, Appl 10 US-09-98-598-904 Sequence 139, Appl 10 US-09-884-76-7873 Sequence 703, Appl 10 US-09-884-76-7073 Sequence 703, Appl 10 US-09-884-76-7073 Sequence 6862, Appl 10 US-09-884-17-1727 Sequence 1727, Appl 10 US-09-764-847-1727	ALIGNMENTS ULT 1 ULT 1 UCP 26-581-5 equence 5, Application US/09826581 atent No. US20020142310A1 ENERAL INFORMATION: ENERAL INCORMATION: ENERAL INCORMATION ENERAL INCORMATION ENERAL INCORMATION ENERAL INCORMATION ENERAL	tch al Similarity 100.0%; Pred. No. 0; al Similarity 100.0%; Pred. No. 0; 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0; TTGGTCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCACCACATGCAGCACCCCTTC 60
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	1-5 Application US US20020142310A1 US20020142310A1 CORMATION:	Similarity 7; Conser GTCTGGGGCT
	RESULT 1 US-09-826-581-5 Sequence 5, Application US/099 Patent No. US20020142310A1 GENERAL INFORMATION APPLICANT: Authman, L. Holge APPLICANT: Marklund, Stefan TILE OF INVENTION: VARIANTS FILE REFERENCE: 11145-007001 CURRENT APPLICATION NUMBER: US PRIOR PILING DATE: 2001-04 PRIOR PELICATION NUMBER: US PRIOR FILING DATE: 2001-04 PRIOR FILING DATE: 2001-04 NUMBER OF SEQ ID NOS: 14 SOFTWARE: PARISEQ for Windows SOFTWARE: PARISEQ for Windows SOFTWARE: PARISES TYPE: DNA ORGANISM: HOMO SADIENB FEATURE: COCCATION: (20)(1486)	Match Local Si es 1647; 1 TTGGT 1 TTGGT
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GENERAL INFOCUENT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TIELE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBURITE ERFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 4.0
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                                   TCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGAGAAGATCTGAG
                                                                                                                               TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAAACTCAGC
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Best Local Similarity 100.0%; Pred. No. 4.2e-191;
Matches 406; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             GGCCATGACACCAGCCTCTTAGTCTTC 1647
                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09826581; Patent No. US20020142310A1; GENERAL INFORMATION:
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US-09-826-581-2
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10.2%; Score 168; DB 10; Length 1722;
Best Local Similarity 100.0%; Pred. No. 2.4e-73;
Matches 168; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                      1142 TTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
                                                                                                                                                                                                                                                                      ; Sequence 3373, Application US/09864761
; Patent No. US20020048763A1
                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3
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US-09-864-761-3373/c
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APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI
FILE REFRENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826,581
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020142310A1

GENERAL INFORMATION:

APPLICANT: Anderson, Leif

APPLICANT: Luthman, L. Holger

APPLICANT: Marklund, Srefan

TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI

FILE REFERENCE: 11145-007001

CURRENT APPLICATION NUMBER: US/09/826,581

CURRENT FILING DATE: 2001-04-05

PRIOR PRIOR APPLICATION NUMBER: US 60/195,665

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 14
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547 GCGCAAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACTGCTACGATGC 606
               917 GAGAACTCAGCCTTCATCTTCCCCCACCCCCATTGCTGGTTCAGCTTTCAGGTAG 976
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                                                       607 CATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAG 652
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                                                                                                                                                           Sequence 4, Application US/09826581
Patent No. US20020143110A1
GENERAL INFORMATION:
APPLICANT: Andersson, Leif
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Best Local Similarity 100.
Matches 278; Conservative
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ORGANISM: Homo sapiens
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US-09-826-581-4
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APPLICANT: Anderseon, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUB
FILE REFERENCE: 11145-007001
CURRENT FILING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-07
NUMBER OF SEQ ID NOS: 14
SOCTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HALLO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BIT4'4, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BIT4'4, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.00e-06
OTHER INFORMATION: WISSPROT HIT: P54619, EVALUE 3.00e-06
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100.0%; Pred. No. 5.9e-17;
iive 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 52; DB 10; I
lilarity 100.0%; Pred. No. 5.8e-16;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Marches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 20146
LENGTH: 92
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US-09-826-581-1
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APPLICANT: Renn, Sharron G.
APPLICANT: Harnel, David R.
APPLICANT: Chen, Wenabheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acenia-X-1
CURRENT APPLICATION NUMBER: US/09/664.761
CURRENT APPLICATION NUMBER: US/09/664.761
PRIOR APPLICATION NUMBER: US/09/613.366
PRIOR APPLICATION NUMBER: US/09/63.366
PRIOR APPLICATION NUMBER: US/09/63.366
PRIOR APPLICATION NUMBER: US/09/63.366
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/09/63.366
PRIOR FILING DATE: 2000-00-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
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                                                                                                                                                                        OTHER INFORMATION: MAP TO ACO09974.3
OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN ABULTO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN ABULT LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BY474, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%; Score 85; DB 10; Length 378, 100.0%; Pred. No. 2.7e-32; ive 0; Mismatches 0; Indels
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 3373
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20146, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 85; Conservative
                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Gaps

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US-09-864-761-22801

Sequence 22801, Application US/09864761

Sequence 22801, Application US/09864761

Sequence 22801, Application US/09864761

Sequence 22801, Application US/09864761

Settle No. US20020048763A1

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04
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Sequence 38, Application US/09832292

Sequence 38, Application US/09832292

Sequence 38, Application US/09832292

Sequence 38, Application US/09832292

GENERAL INFORMATION

TITLE OF INVENTION: DIAGNALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND TITLE OF INVENTION: DIAGNASTIC AND THERAPEUTIC USES THEREOF

TITLE OF INVENTION: DIAGNASTIC AND THERAPEUTIC USES THEREOF

CURRENT APPLICATION NUMBER: US/09/832,292

CURRENT FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: 09/632,131

FRIOR APPLICATION NUMBER: 09/632,131
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100.0%; Pred. No. 12;
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100.0%; Pred. No. 13;
ive 0; Mismatches 0; Indels
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                               TELECOMMUNICATION INFORMATION
TELEPHONE: 703-413-3000
TELEPKX: 703-413-220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 7771
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Best Local Similarity 100.0%
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-09-832-292-38
                                                                                                                                                                                                                                                                                         NAME/KEY:
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Best Local Similarity
Matches 19; Conserv
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
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0
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APPLICANT: HIRANO, NISHINOMIYA
TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
PRE-B CELL GROWTH-SUPPORTING ABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 20; DB 10; Length 333;
100.0%; Pred. No. 3.9;
ive 0; Mismatches 0; Indels
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                   Sequence 1402, Application US/09974300
Faten No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Wethods For Monitoring Multiple Gene
TITLE OF INVENTION: WOMBER: US/09/974,300
CURRENT APPLICATION NUMBER: US/08/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR PELICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-00-66
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,720
FILING DATE: 24-Aug-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/517,739
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/997,252
FILING DATE: 23-DC-1997
APPLICATION NUMBER: US 08/537,942
FILING DATE: 21-NOV-1995
APPLICATION NUMBER: DCT/JP94/00819
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: DCT/JP94/00819
FILING DATE: 21-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09935720; Patent No. US20020156260A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA

CRGANISM: Bacillus licheniformis
US-09-974-300-1402
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COMPUTER READABLE FORM:
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Matches 20; Conserv
US-09-974-300-1402
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US-09-935-720-2
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Gaps

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Sequence 6044, Application US/09864761
Parent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Howenshong;
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL PO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILLE REPRENSE. Accomica-X-1
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| Patent No. US20020132237A1
| Patent No. US20020132237A1
| GENERAL INFORMATION:
| APPLICANT: AJlate, Paul A.
| APPLICANT: AJlate, Robert
| APPLICANT: AJlate, Robert
| APPLICANT: AJlate, Robert
| TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
| FILE REFERENCE: 210121.497 | CURRENT FILING DATE: 2001-05-29 |
| NUMBER OF SEQ ID NOS: 10912 |
| SOFTWARE FEALSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 18; DB 10; Length 325; Best Local Similarity 100.0%; Pred. No. 39; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                              LOCATION: (240)
OTHER INFORMATION: ungure at all n locations
OTHER INFORMATION: Clone ID: 11-LIB3058-018-01-K1-C3
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                          FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2438
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CURRENT FILING DATE: 2001-05-23
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; LOCATION: (1)...(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-968
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ORGANISM: Homo sapien
                                                                                                                                                                                                                         TYPE: DNA ORGANISM: BOS taurus
                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-867-701-968/c
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, John C.
APPLICANT: Mathialagan, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EST HUMAN HIT: AW749933.1, EVALUE 2.00e-71
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100.0%; Pred. No. 38;
tive 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-3
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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PRIOR PLILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
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PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2001-01-30
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Patent No. US20020137139A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Matches 18; Conserv
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US-09-864-761-22801
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1.1%; Score 18; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                     PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
LENGTH: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 GCCACAGAGGCCTGGGAG 457
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                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-230
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Job time: 492.092 secs
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1.1%; Score 18; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PELING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-04
PRIOR PELING DATE: 2000-00-07
PRIOR PELING DATE: 2000-00-07
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003104.1
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Sequence 230, Application US/09962436
Parent No. US20020081301A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
PRIOR APPLICATION NUMBER: US/60/235,082

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                                                                                                     January 6, 2003, 20:16:02; Search time 62.0864 Seconds (without alignments) 8135.386 Million cell updates/sec
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-470-1189-
US-08-194-981E-4
US-08-660-963-9
US-09-101-146-63
US-08-194-981E-3
US-08-646-273-18
US-08-231-118-10
US-08-2318-8218-10
US-08-2318-8218-10
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US-08-218-8218-4
US-08-646-273-22
US-08-646-273-22
US-09-104-318-9
US-09-104-318-9
US-09-118-628-17
US-09-018-628-17
US-09-018-635-26
US-09-018-635-26
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                                                                         - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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28 17 1.0 4127 4 US-09-487-168A-10 Sequence 10, Appl c 29 17 1.0 6453 1 US-08-306-691B-14 Sequence 14, Appl c 31 17 1.0 6453 3 US-09-209-668-10 Sequence 10, Appl c 31 17 1.0 6453 3 US-09-56-20 Sequence 3, Appl c 31 17 1.0 9551 1 US-08-056-200-93 Sequence 93, Appl c 31 17 1.0 9551 2 US-08-001-644-93 Sequence 93, Appl c 31 17 1.0 28473 4 US-09-325-936-60 Sequence 60, Appl c 35 17 1.0 28473 4 US-09-784-250 Sequence 3, Appl c 37 1.0 28473 4 US-09-784-316-3 Sequence 3, Appl c 37 1.0 11228 4 US-09-784-316-3 Sequence 3, Appl c 37 1.0 111229 4 US-09-784-316-3 Sequence 1, Appl c 39 17 1.0 411529 4 US-09-10-840A-1 Sequence 1, Appl c 1.0 111529 4 US-09-10-840A-1 Sequence 1, Appl c 1.0 111529 4 US-09-10-840A-1 Sequence 1, Appl c 1.0 1122 4 US-09-10-840A-1 Sequence 1, Appl c 1.0 116 1.0 284 105-0-536-421-15 Sequence 19, Appl c 1.0 146 3 US-08-510973A-19 Sequence 19, Appl c 1.0 146 3 US-08-548-91-9 Sequence 19, Appl c 1.0 239 3 US-08-756-340-9 Sequence 47, Appl c 1.0 239 3 US-08-756-849-47 Sequence 47, Appl c 1.0 239 3 US-08-756-849-94 Sequence 47, Appl c 1.0 239 3 US-08-756-849-94 Sequence 47, Appl c 1.0 239 3 US-08-756-849-94 Sequence 47, Appl c 1.0 230 2 US-08-756-849-94 Sequence 47, Appl c 1
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ALIGNMENTS

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Sequence 2. Application US/08537942A

Patent No. 5753464

GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
APPRESSEE: P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: UA
ACOUNTRY: USA
APPLICATION NUMBER: US/08/537,942A
FILING DATE: 21-MAY-1994
APPLICATION NUMBER: DATA
APPLICATION NUMBER: JA 5-141178
FILING DATE: 21-MAY-1994
APPLICATION NUMBER: JA 5-141178
FILING DATE: 21-MAY-1994
APPLICATION NUMBER: JA 5-141178
FILING DATE: ALIBRADO ACOUNTRY ATTON NUMBER: JA 1619
ATTONBEY/AGENT INFORMATION:
APPLICATION NUMBER: JA 1619
ATTONBEY/AGENT INFORMATION:
ATTONBEY/AGENT INFORM
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us-09-826-581-5.oligo.rni

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948 ACAGCACCCATCCTGACTG 966
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                          Query Match
1.2%; Score 19; DB 1; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels
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1.2%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08997252A
Patent No. 6232453
GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,252A
FILING DATE: 23-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,942
FILING DATE: 21-MOV-1995
FILING DATE: 21-MAY-1994
FILING DATE: 20-MAY-1994
FILING DATE: 20-MAY-1994
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET UNBER: 4767-0005-0 PCT
TELEPHONE: 703-413-3000
TMENDRATION FOR SET 170.007-
                                                                                                                                           1112 ACAGCACCCATCCTGACTG 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1411 base pairs TYPE: nucleic acid STRANEDNESS: double
                                                                                                                                                                   948 ACAGCACCCATCCTGACTG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
      ; OTHER INFO
US-08-537-942A-2
                                                                                                                                                                                                                                               RESULT 2
US-08-997-252A-2
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US-09-517-739-2

Sequence 2, Application US/09517739

Fatent No. 6370723

GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO

TITLE OF INVENTION: GENE ENCODING A POLYBEPTIDE HAVING A

TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

CTTY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : NAME/KEY: sig_peptide

: LOCATION: 1..84

: OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-09-517-739-2
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,739
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/997,252
FILING DATE: 21-DEC-1997
FILING DATE: 21-NOV-1995
PRIOR APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 20-MAY-1994
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 19; DB 4;
ilarity 100.0%; Pred. No. 12;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    948 ACAGCACCCATCCTGACTG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserva
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RESULT 4 US-08-470-179-189/c

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Gaps

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Indels

1112 ACAGCACCCATCCTGACTG 1130

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RESULT 6
US-06-660-963-9
Sequence 9, Application US/08660963
Sequence 9, Application US/08660963
Setent No. 5852187
GENERAL INFORMATION:
APPLICANT: Thorner, Michael O.
APPLICANT: Horikawa, Reiko
APPLICANT: Lyons Jr., Charles E.
ITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
ITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
ITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
ITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
ITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
STREET: METOPOLITAN SQUARE BUILDING, SUITE 800, 1450
STREET: Mashington
STREET: Washington
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.0%; Score 17; DB 2; Length 1419; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,981E
FILING DATE: Pebruary 10, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Selby
REGISTRATION NUMBER: 22000.0022
TELEFONE: (404) 689-980
TELEFONE: (404) 689-980
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1419 base pairs
TYPE: MICHAEL ASINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,963
FILING DATE: 12-JUN-1996
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NAME: O'Shaughnessy, Brian P.
REGISTRATION NUMBER: 32,747
REFERENCE/DOCKET NUMBER: 18046.036
TELEPHONE: 202-824-8000
TELEFRAX: 202-824-8199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO
US-08-194-981E-4
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Sequence 189, Application US/08470179

Batent No. 5645994

GENERAL INFORMATION:

TITLE OF INVENTION: Method and Compositions for TITLE OF INVENTION: Method and Compositions for TITLE OF INVENTION: Identification of Species in a Sample CORRESPONDENCE ADDRESS: 207

CORRESPONDENCE ADDRESS:

ADDRESSEE: Trask, Britt and Rossa
STREET: Usah

CONTRY: Salt Lake City
STATE: Usah

COUNTRY: Usah

COUNTRY: Usah

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CLASSIFICATION NUMBER: US/08/470,179

FILING DATE:

CLASSIFICATION UNBER: 36,289

REFERENCE/DOCKET NUMBER: 2601

TELECOMMUNICATION INFORMATION:

TELEPHONE: NUMBER: 2601

TELECOMMUNICATION INFORMATION:

TELEPHONE: 001-53-1922
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
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Patent No. 5886157

GENERAL INFORMATION:
APPLICANT: GUO, ZUYU
APPLICANT: GUO, ZUYU
APPLICANT: GILLAM, Elizabeth M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
TITLE OF INVENTION: CYTOCHROME P450
TITLE OF INVENTION: CYTOCHROME P450
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: STILE 1200, 127 Peachtree Street, NB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOLING
NATI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 801-531-9168
INPORMATION FOR SEQ ID NO: 189: SEQUENCE CHARACTERISTICS: LENGTH: 423 base pairs TYPE: nucleic acid STRANDEDRESS: double TOPOLOGY: not relevant MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCAGGACCCCTTCCTGG 45
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Matches 17; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM:
US-08-470-179-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-194-981E-4
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Gaps

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HYPOTHETICAL: N; ANTI-SENSE: NO US-08-194-981E-3
RESULT 8
US-08-194-981E-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/09101146
Parent No. 6124125
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: 50e Massey Licata, Esq.
STREET: 66 E. Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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.00.0%; Pred. No. 1.1e+02;
.ve 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TIPE: DISKETIE, 3.5 INCH, 1.44 MD
COMPUTER: 18M PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDERFECT 6.0 FOR WINDOWS
SOFTWARE: WORDERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/09/101,146
FILING DATE: October 7, 1998
FILING DATE: OCTOBER 1, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%; P. Conservative 0;
                                      LENGTH: 1545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 GAGGCCTGCCCTGTGCC 500
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TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 1..1371
US-08-660-963-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Marlton
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-101-146-63
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Matches
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Gaps

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Sequence 10. 34 Application US/08238821B

Facent No. 5912120

GENERAL INFORMATION:
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: COMMES-SPRAKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF STATES OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF STATES OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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                                                               Length 1852
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for 65 of Figure 2."
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1.0%; Score 17; DB 2; Length 1852;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,8218

TITING DATE: 06-MXY-1994
                                                            Query Match 1.0%; Score 17; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICR APPLICATION DATA:
PRICR APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTAATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-19211
TELECOMMUNICATION INFORMATION:
TELEFAN: (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                    Qy 1266 GTGTGGGAGAGCCCTG 1282
                                                                                                                                                                                                                   Db 1314 GrGrGGGAGAGCCCTG 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1266 GTGTGGGAGAAGCCCTG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Region
LOCATION: 1..10
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        US-08-238-821B-10
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             US-08-201-118-10
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Sequence 10, Application US/08201118

Parent No. 5786191

Parent No. 5786191

Parent No. 5786191

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROWKES-SPARKS, Marjorie

TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: SUBFAMILY

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage COMPUTER: IBM AT-compatible, 80486 processor oPERATIOS SYSTEM: MS-DOS veraion 6.0 SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,273 FLING DATE: 16-NOV-1994 CLASSIFICATION NUMBER: PCT/EP94/03706 FILING DATE: 11-NOV-1994 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 1703 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: A PACHILIN RELEASE #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
1.0%; Score 17; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-192-1
TELECHONINICATION INFORMATION:
TELEFAX: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
; MOLECULE TYPE: CDNA for mRNA
US-08-646-273-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      983 CTGGAGATCAAGAAGGC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647 CTGGAGATCAAGAAGGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SD
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Gaps

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APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROWKES-SPARKS, Marjorie
APPLICANT: ROWKES-SPARKS, Marjorie
APPLICANT: ROWES-SPARKS, Marjorie
APPLICANT: DE MORAIS, SONIA M.F.
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
TITLE OF INVENTION: MEPHENYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                     NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 05-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1; Le
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15280-192-1
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FILING DATE: 06-MAY-1994
                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08238821B Patent No. 5912120 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFRENCE/DOCKET NUMBER: 1528(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TITLE OF INVENTION: SUBFAMILY
                                                                                              379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1266 GTGTGGGAGAGCCCTG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                              STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-201-118-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94111
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US-08-238-821B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
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Sequence 4, Application US/08201118

Sequence 4, Application US/08201118

Patent No. 5786191

Patent No. 5786191

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: GOLDSTEIN, Joyce A.

TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: DNAB FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                   APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: DE MORNIO.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
CORRESPONDENCES 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 1.18+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REBERBENCE/DOCKET NUMBER: 15280-192-1-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1852 bass pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION NUMBER: US 08/201,118
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                              PCT-US95-05744-10
Sequence 10, Application PC/TUS9505744
GENERAL INFORMATION:
1314 GTGTGGGAGAAGCCCTG 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1266 GTGTGGGAGAGCCCTG 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear HOLECULE TYPE: CDNA PCT-US95-05744-10
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                                                                         RESULT 12
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Gaps

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PCT-US95-05744-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GOLDSTEIN, Joyce A.
APPLICANT: ROMKES-SPARKS, Marjorie
APPLICANT: DE MORAIS, Sonia M.F.
TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
TITLE OF INVENTION: OF S-MEPHYNYTOIN METABOLISM
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 3.79 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Corresponds to positions -12 to-1 for 25 of Figure 2."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 17; DB 2; Length 1854; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: 104 Louisend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURETY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05744
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
CLASSIFICATION NUMBER: US 07/864,962
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/864,962
FILING DATE: 09-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 15280-192110US
REFERENCE/DOCKET NUMBER: 15280-192110US
TELEPHONE: (650) 326-2400
TELEPAX: (650) 326-2400
TELEPAX: (650) 326-242
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: LINCARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
TYPE: Inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,821
FILING DATE: 06-MAY-1994
PRIOR APPLICATION NUMBER: US 08/201,118
FILING DATE: 22-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-05744-4
; Sequence 4, Application PC/TUS9505744
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1316 GTGTGGGAGAGCCCTG 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.08
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..12
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Region LOCATION: 1..12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-238-821B-4
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Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months According to the Pre Publication Rules, every patent application received by the United States from the effective filing date. When the application is published the contents, including th sequences, will become prior art.

Published_Applications_NA contains nucleic acid sequences; the search results will have the Two new databases have been created to hold the pre-published sequences: extension .rnpb.

Published_Applications_AA contains amino acid sequences; the search results will have the extension .rapb

requests that the changed application be published again. In such instances, the "1" at the end of beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application. The first 4 digits show the calendar year the application was published. The next digits represent when the application was published. This 7-digit number starts at zero at the application had been published. If the applicants submit changes to the application, they may Publication Number is US20021234567A1. The "US" indicates the application was a U.S. Each pre-published application is given a unique Publication Number. An example of a the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to results in the case.

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Sequence 5, Appli
Sequence 20146, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 36, Appli
Sequence 362, Appl
                                                                                             January 6, 2003, 17:17:03 ; Search time 500.908 Seconds (without alignments) 1486.844 Million cell updates/sec
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                                                                                                                                                                                                     1 cctggcccctcagatcaaga.....gatgagaggctcgggctgga 1722
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/DS07_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 3, Application US/09826581

Sequence 3, Application US/09826581

Sequence 3, Application US/09826581

Sequence 3, Application US/09826581

Sequence 3, Application US/0826581

Sequence 3, Application Light Carlos Used Carlos Carl
                                                                      Sequence 362, App
Sequence 65, App
Sequence 67, App
Sequence 21, App
Sequence 7, Appl
Sequence 7, Appl
Sequence 11329, A
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Sequence 3, Appli
Sequence 294, App
Sequence 2401, Ap
Sequence 22801, A
Sequence 2638, Ap
Sequence 604, Ap
Sequence 604, Ap
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68, Appl
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                                                   Sequence
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 1722, Conservative
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459
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ORGANISM: Homo sapiens
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Oy 241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300 Db 241 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300	36	OY 361 AGCAAATGGGGGAGGCAGGAGAAAAGAGCCCCACTTCTCAGGCCTGGGGGGCTGCCCC 420 bb 361 AGCAAATGGGGGAGGCAGGAGAAAGAGCCCCACTTCTCAGGCCTGGGGGGCTGCCCC 420	8 4	5 54 5		601 GGTCCCCCTGGTGAGGAGTGGGCAAATCTTATGGGCACCCGAGGGGCGGGGGG 66	661	721 CTGTCGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACAAGATTGAGACTGGAG 78 	781 GGGTGAGTGGGGAGAGGAACCCGGAAAGGGGCTGTTGGTGGTGGGCCAGGGCTTAAG 84 	841 GTGGAGGATGGGCAGTGGGGATGTCCTGGAGTGAACAGGGGACAATAGGAGCCTCG 9	901 GGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGGTGACGTGACCGGCTCCC 96	961 IGGCCTGACTCTGGCTCTTTCTGCAGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGT 10	1021 CTCCATCTCCTAATGATAGGTGGTGTCTCTGCTCATTCACCTGAGCCTCCTCCC 10	1081 ACAGTCCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACCTCTTCATCCTAGGCGGCACA 114	1141 CAGACAAGGGAGCCTTGGTGCCCTGCCTTTTTAGGGGCCTGGATGGA	1201	1261	1321 ACTCCACATCCTCACACACACACCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG 138
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REPRIZAM: PERMENATION: A US 200.0004 876.31

REPREZAM: PERMENATION: A US 200.0004 876.31

REPLICANT: PERMENATION: A PROPERTY OF THE PERMENATION: A PRELICANT: HARDEL, DAVIG R.

A PRELICANT: HARDEL, DAVIG R.

A PRELICANT: CHEN, WENTERSON GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUWAN GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT PRILICATION NUMBER: US /09/664, 761

PRIOR FILIR DATE: 2000-02-04

RECORDER APPLICATION NUMBER: US /09/662, 366

PRIOR PRILICATION NUMBER: US /09/664, 766

PRIOR APPLICATION NUMBER: US /09/664

PRIOR PRILICATION NUMBER: 08/60.20

PRIOR PRILICATION NUMBER: 08/60.20

PRIOR PRILICATION NUMBER: POTUSO1/0066

PRIOR PRILICATION NUMBER: POTUSO1/0067

PRIOR PRILICATION NUMBER: POTUSO1/00670

PRIOR PRILICATION NUMBER: POTUSO1/00670

PRIOR PRILICATION NUMBER: POTUSO1/00670

PRIOR PRILICATION NUMBER: POTUSO1/00670

PRIOR PRILICATION NUMBER: POTUSO1/00670
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                         1523 GGTTCCCTGCTGCCCGGCCCTCCTTCCTACCGCACTATCCAAGATTTGGGCATCGGC 1582
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                                                                                                                                                                                                                                                                                                                        1022 GGTTCCCTGCTGCCCCGGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1081
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                                                                                                                                                                                            Length 1647;
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100.0%; Pred. No. 3.1e-72;
ive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELLING DATE: 2001-05-23
PRIOR PELLING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-06
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2001-01-04
PRIOR PELLING DATE: 2001-01-30
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R APPLICATION NUMBER: US 60/234,687

R FILING DATE: 2000-09-21

R FILING DATE: 2000-06-30

R FLING DATE: 2000-06-30

R APPLICATION NUMBER: US 09/774,203

R FILING DATE: 2001-01-29
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 168; Conservative
                                                                         ; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
                      ORGANISM: Homo sapiens
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US-09-826-581-5
US-09-826-581-5
Sequence 5, Application US/09826581
Fatent No. US20020142310A1
Fatent No. US20020142310A1
FAPPLICANT Andersson, Leif
APPLICANT Luthman, L. Holger
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNI CURRENT FILING DATE: 2001-04-05
FILE REFERENCE: 11145-007001
CURRENT FILING DATE: 2000-04-07
FRIOR APPLICATION NUMBER: US 60/195,665
FRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GGAGTCTGCATGGCCAGCTGGAGCCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT 300
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                                                                                                                                                                                                                                    CREATURE:

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN HELAFT, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN PT474, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.3

OTHER INFORMATION: EXPRESSED IN BOWE MARROW, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8

US-09-864-761-3373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGC 17
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PRILOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 3373
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Gaps
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 0.78

OTHER INFORMATION: SWISSPROT HIT: P32595. EVALUE 7.60e-01

OTHER INFORMATION: NI HIT: AFI46793.2, EVALUE 4.40e-01

US-09-864-761-27246
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100.0%; Pred. No. 15;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us-09-092-296-2/c

i Sequence 2, Application US/09092296

j Publication No. US20020188114A1

GENERAL INFORMATION:
APPLICANT: BILLING-NEDEL, PATRICIA
APPLICANT: COHEN, MAUNICE
APPLICANT: COHEN, PAULA N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RISEMAN, PAULA N.
APPLICANT: RISEMAN, PAULA N.
APPLICANT: RISEMAN, PAULA N.
TITLE OF INVENTION: STROUPE, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
STRFFT:
STRFTT:
S
                                                              PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PILICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PAPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEC for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Abbott Laboratories
1: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1232 CATCTCTGCAGCCTGTTTG 1250
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                                            2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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Patent No. US20020048763A1
Patent No. US20020048763A1
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 CCTGGCCCCTCAGATCAAGAGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC 6
                                                                                                                                                  PER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HELACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BALIO, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN BAT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BOLE 2.00e-22
OTHER INFORMATION: EXPRESSED IN BALAN, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BALAN, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BALAN, SIGNAL = 3.00e-06
OTHER INFORMATION: SWISSPROT HIT: BB327467.1, EVALUE 3.00e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 3.8%; Score 65; DB 10; Length 92; Best Local Similarity 100.0%; Pred. No. 5.3e-22; Matches 65; Conservative 0; Mismatches 0; Indels
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20146
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILLE REFERENCE: Acomica.x.1

CURRENT APPLICATION NUMBER: US/09/664,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-07

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-20146
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                                                                   APPLICANT: COLPITS, TRACEY L.
APPLICANT: COLPITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUGE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL,
TITLE OF SEQUENCES: 20
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 19; DB 9; Length 389; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels
                                                                                                                                                                                               Length 239;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FestSep for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
                                                                                                                                                                                             Query Match 1.1%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 15; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 60/048,810
ATTORNEY/AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09092296
; Publication No. US20020188114A1
; Publication No. US20020188114A1
; Publicant: BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                       226 TGAAGGGAGATGGAGGAGG 208
                                                                                                                                                                                                                                                                               116 TGAAGGGAGATGGAGGAGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TGAAGGGAGATGGAGGAGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 847/938-2623
  STRANDEDNESS: sit
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-092-296-5
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-092-296-5/c
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APPLICANT: COHEN, MAURICE
APPLICANT: COLFITS, TRACEY L.
APPLICANT: RIBDMAN, PAULA N.
APPLICANT: RIBSELL, JOHN C.
APPLICANT: RISSELL, JOHN C.
APPLICANT: STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDOLT LADORATORIES
                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 229;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 19; DB 100.0%; Pred. No. 15; tive 0; Mismatches
                          NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104.US.01
TELECOMMUICATION INFORMATION:
TELEPHONE: 847/938-2623
TELERX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park Road STATE: 1L COUNTRY: USA ZIP: 6064-1500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
CLASSIFICATION:
PILOR APPLICATION
APPLICATION DATA:
PILING DATE:
O5-UN-1997
ATONEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104.US.
TELECOMMUNICATION INFORMATION:
TELECHONE: 847/935-1729
APPLICATION NUMBER: 60/048,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09092296
Publication No. US20020188114A1
GENERAL INFORMATION:
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2.29 base pairs : TYPE: mucleic acid : STRANDEDNESS: single : TOPOLOGY: linear US-09-092-296-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 TGAAGGGAGATGGAGGAGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 TGAAGGGAGATGGAGGAGG 204
          FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker Cherri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 847/938-2623
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PAPELLAWY: Zhang Camina I.

APPLILAWY: Zhang Zamin II.

TITLE OF INVENTION: Acid Brickling the Same Colypeptides and Nucleic III. OF PRINKING No. Acid Brickling the Same Colypeptides and Nucleic III. OF INVENTION: Acid Brickling the Same Colypeptides and Nucleic III. REFERENCE: P3730FC20

CURRENT FILING DATE: 2000-11-14

PRIOR PAPLICATION NUMBER: 60/604970

PRIOR APPLICATION NUMBER: 60/604970

PRIOR PAPLICATION NUMBER: 60/60511

PRIOR PAPLICATION NUMBER: 60/60511

PRIOR PAPLICATION NUMBER: 60/60510

PRIOR PAPLICATION NUMBER: 60/60500

PRIOR PAPLICATION NUMBER: 60/
                                                                                                             Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
                                                                                                                                                                                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                    Ferrara, Napoleone
                                                                   Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                         Paoni, Nicholas F.
                                                                                                                                                                                         Gurney, Austin L.
                                                                                                                                                                                                                   Kljavin, Ivar J
                                                                                                                                                                                                                                          Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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0
                                                                                                                                                                                                           APPLICANT: COHEN, MAURICE
APPLICANT: COHEN, MAURICE
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITYS, TRACEY L.
APPLICANT: RISEDMAN, PAULA N.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 19; DB 9; Length 413; 100.0%; Pred. No. 15;
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MEDIUM TYPE: Diskette COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPUTER: DISKETTE COMPUTER: DOS SOFTWARE: FastSRO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
FILING DATE: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00/048,810
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BECKET. CHEYJL L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104.US.01
TELECHOWNICATION INFORMATION:
TELECHOWNICATION INFORMATION:
TELEFHONE: 847/938-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
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Publication No. US20020188114A1
GENERAL INFORMATION:
196 TGAAGGGAGATGGAGGAGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 TGAAGGGAGATGGAGGAGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 rgaaggaargaagagg 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEO ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 19; Conservative
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US-09-092-296-6
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                                                                                                RESULT 9
US-09-092-296-6/c
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60/090445

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PRIOR APPLICATION NUMBER: 60/08855
PRIOR APPLICATION NUMBER: 60/08855
PRIOR FILING DATE: 1998-06-05
PRIOR PELICATION NUMBER: 60/08855
PRIOR PELICATION NUMBER: 60/088742
PRIOR PELICATION NUMBER: 60/08824
PRIOR PELICATION NUMBER: 60/08824
PRIOR PELICATION NUMBER: 60/08824
PRIOR PELICATION NUMBER: 60/08826
PRIOR PELICATION NUMBER: 60/08926
PRIOR PELICATION NUMBER: 60/08926
PRIOR PELICATION NUMBER: 60/08926
PRIOR PELICATION NUMBER: 60/08926
PRIOR PELICATION NUMBER: 60/08929
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100.0%; Pred. No. 15;
tive 0; Mismatches 0; Indels
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PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
                                         NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090535

NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090540

NR FILING DATE: 1998-06-24

NR APPLICATION NUMBER: 60/090542

NR APPLICATION NUMBER: 60/090542
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Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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Godowski, Paul J.
Grimaldi, J. Christopher
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Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 100.
Matches 19; Conservative
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088824
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088824
R FILING DATE: 1998-06-10
                                                                                                                                                                                                                   R APPLICATION NUMBER: 60/088858
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
F FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088976
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/089514

R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R FILING DATE: 1998-06-17

R FLING DATE: 1998-06-17
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089653
R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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                                                 PRIOR
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APPLICANT: WOOD, WILLIAMS, P. MILLAMS, P. 
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APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
                                                                            Paoni, Nicholas F.
Roy, Margaret Ann
Stewart. Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Gurney, Austin L.
                      Kljavin, Ivar J.
                                        Napier, Mary A.
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APPLICANT:
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Gaps

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                 Length 422;
                                                                                                                                                        0; Indels
                                                                                           core 19; DB 9; Pred. No. 15; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
                                                                                                 Score 19;
Pred. No.
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PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-20
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PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR PRIOR DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-989-735-362/c
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
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100.0%; Pre
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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Grimaldi, J. Christopher
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FILING DATE: 1998-06-02
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                        234 TGAAGGGAGATGGAGGAGG 216
                                                                                                                                                                                                      116 TGAAGGGAGATGGAGGAGG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara, Napoleone
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Goddard, Audrey
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                                                                                        Query Match
Best Local Similarity 100.
Matches 19; Conservative
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Stewart, 11...
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           ; ORGANISM: Homo Sapien
US-10-063-547-65
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APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerriteen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT
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Mismatches
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100.0%; Pred. No.
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OR APPLICATION NUMBER: 60/090695
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OR APPLICATION NUMBER: 60/091780
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090678
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
                                                                                   60/090557
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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Publication No. US20020182638A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 19; Conservative
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PRIOR APPLICATION NUMBER: 60/08952
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/09167
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1.1%; Score 19; DB 9; Length 422; 100.0%; Pred. No. 15; iive 0; Mismatches 0; Indels

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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088658
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08861
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R APPLICATION NUMBER: 60/088030
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A PAPLICATION NUMBER: 60/088033
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R APPLICATION NUMBER: 60/088217
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R APPLICATION NUMBER: 60/088810
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R FILING DATE: 1998-06-17
R APPLICATION NUMBER: 60/089538
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-19
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APPLICANT: Watlanbe, Colin K.
APPLICANT: Watlanbe, Colin K.
APPLICANT: Walliam I.
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: P2710PLCJ
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT APPLICATION NUMBER: US/09/980,980
PRIOR FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: US/09/990
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR PELLOR CATION NUMBER: US/09/9910
PRIOR APPLICATION NUMBER: US/09/9910
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US/08/960
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
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Publication No. US20020193300A1
GENERAL INFORMATION:
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                        234 TGAAGGGAGATGGAGGAGG 216
116 TGAAGGGAGATGGAGGAGG 134
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Napier, Mary A.
Pan, James
Paoni, Nicholas F.
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
PRIOR APPLICATION NUMBER: 60/049787
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30 A PAPLICATION NUMBER: 60/049787

30 R FILING DATE: 1997-06-16

31 A PAPLICATION NUMBER: 60/062250

32 R FILING DATE: 1997-10-17

33 A PAPLICATION NUMBER: 60/065186

34 A PAPLICATION NUMBER: 60/065311

35 A PAPLICATION NUMBER: 60/065311

36 A PAPLICATION NUMBER: 60/065311

37 A PAPLICATION NUMBER: 60/065310

38 FILING DATE: 1997-11-24

39 R FILING DATE: 1998-02-25

38 A PAPLICATION NUMBER: 60/078910

39 R FILING DATE: 1998-04-28

38 A PAPLICATION NUMBER: 60/084600

38 A PAPLICATION NUMBER: 60/084500

39 R FILING DATE: 1998-06-02

30 R A PAPLICATION NUMBER: 60/084106

30 R A PAPLICATION NUMBER: 60/084500

30 R A PAPLICATION NUMBER: 60/087106

31 A PAPLICATION NUMBER: 60/087106

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36 A PAPLICATION NUMBER: 60/087507

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38 A PAPLICATION NUMBER: 60/087507
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R FILING DATE: 1998-06-03
R FILING DATE: 1998-06-04
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R FILING DATE: 1998-06-07
          Application US/09989730 o. US20020197674A1
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088028
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
Tumas, Daniel
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Fong, Sherman
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Gerritsen, Mary E.
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Botstein, David
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100.0%; Pred. No. 15;
ive 0; Mismatches (
R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090254

R PILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090355
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R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090444
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090472
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

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R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/090863
R FILING DATE: 1998-06-26
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BR FILING DATE: 1998-07-02
BR APPLICATION NUMBER: 60/091633
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BR APPLICATION NUMBER: 60/091978
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BR APPLICATION NUMBER: 60/091982
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BR APLICATION NUMBER: 60/092182
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090557
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Best Local Similarity 100.
Matches 19; Conservative
PRIOR PRIOR
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FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04

APPLICATION NUMBER: 60/088033

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029

234 TGAAGGGAGATGGAGGAGG 216

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RESULT 15 US-09-989-730-362/c

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PRIOR PLILING DATE: 1998-06-04
PRIOR PAPLICATION NUMBER: 60/08316
PRIOR PAPLICATION NUMBER: 60/08316
PRIOR PAPLICATION NUMBER: 60/08317
PRIOR PAPLICATION NUMBER: 60/08318
PRIOR PAPLICATION NUMBER: 60/08328
PRIOR PAPLICATION NUMBER: 60/083518
PRIOR PAPLICATION NUMBER: 60/08
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PRIOR APPLICATION WIMBER: 60/09429
PRIOR APPLICATION WIMBER: 60/09431
PRIOR APPLICATION WIMBER: 60/09435
PRIOR PILING DATE: 1998-06-24
PRIOR APLICATION WIMBER: 60/09445
PRIOR PILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR APPLICATION WUMBER: 60/09054
PRIOR PLING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION WUMBER: 60/09069
PRIOR PLING DATE: 1998-07-02
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PRIOR PLING DATE: 1998-07-02
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PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION WUMBER: 60/09154
PRIOR PLING DATE: 1998-07-03
PRIOR APPLICATION WUMBER: 60/09154
PRIOR PLING DATE: 1998-07-03
PRIOR APPLICATION WUMBER: 60/09154
PRIOR PRILICATION WUMBER: 60/09154
PRIOR PLING DATE: 1998-07-07
PRIOR PRILICATION WUMBER: 60/09153
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07

Query Match 1.1%; Score 19; DB 9; Length 422; Best Local Similarity 100.0%; Pred. No. 15; Matches 19; Conservative 0; Mismatches 0; Indels 0;

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Search completed: January 7, 2003, 20:17:30 Job time: 506.908 secs

score:

Title: Perfect

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Run on:

Scoring table:

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AA250110 mx79f07.r
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BI775360 467815 MA
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1 (bases 1 to 413)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizaman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,W., W., Wole,B., Schellenberg,K., Steptoe,M., Tan,P., Theising,B., Watte,Y., Wylie,T., Waterston,R. and Wilson,R., Theising,B., Wahle,Y. Thouan EST Project
Contact: Wilson RK
   AW812746 RC3-ST018
                                                                                                                         CIT-HSP-217
                                                                                                                                  AQ291862 nbxb0040M
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1280 Std Brror: 0.00
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2p38410.r1 Stratagene muscle 937209 Homo saphens cDNA clone IMAGE:611731 5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED PROTEIN KINASE, GAWMA CHAIN ;, mRNA sequence.
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H444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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AW8122884 RC3-ST018
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       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Score

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AW812866
RC3-ST0186-300100-017-b03 ST0186 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-300
100-017-b03&t3=2000-01-30&t4=1)
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/clone lib="ST0186"

/dev stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

190 c 151 g 124 t lothers
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                          Length 572;
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2.9e-06;
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2.2%; Score 38; DB
Best Local Similarity 100.0%; Pred. No. 2.9
Matches 38; Conservative 0; Mismatches
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High quality sequence start: 33
High quality sequence stop: 542.
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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 30-JUL-2001
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1543 CTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGCACTTCCGAGACTTGGCTGT 1602
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B1344227
B1344527.1 G1:15037807
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Le
2.8e-22;
Seg primer: -28M13 rev2 from Amersham High quality sequence stop: 255. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No.
                                                          1. .413
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/db_xref="GDB:4643570"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73;
Pred. No.
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Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 572
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/lab_host="DH10B"
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and -minmatch 12 options.
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                                      FEATURES
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DEFINITION

RESULT 4 AW812884

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ACCESS ION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS MEDLINE COMMENT

JOURNAL

TITLE

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 632)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Mataukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dbo=lib="ST0186"
/dov stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-181
099-012-h08&t3=1999-10-18&t4=1)
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Bikaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bikaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

(bases 1 to 655)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Mataukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW812747 655 bp mRNA linear EST 17-MAY-2000
RC3-ST0186-181099-012-d11 ST0186 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                             sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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145 c 157 g 160 t
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High quality sequence stop: 630.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
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               SOURCE
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/db xref="taxon:9606"
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/delw_stage="Adult"
/note="Organ: stomach; Vector: pucl8; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
10 a 125 c 142 g 149 t
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 576)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneal, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-300
100-017-h03&t3=2000-01-30&t4=1)
                                                                                                                                                                              AW812884 570186-300100-017-h03 ST0186 Homo sapiens CDNA, mRNA sequence.
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mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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100.0%; Pred. No. 2.5;
ive 0; Mismatches 0; Indels
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RC3-ST0186-181099-012-h08 ST0186 Homo sapiens cDNA,
AW812763
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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High quality sequence start: 13
High quality sequence stop: 576.
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473 CCTGGGGCTCAATTTCCCCATCTGT 497
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EST.
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Gaps ö

> Query Match Local

Matches

BASE COUNT

ORIGIN

AW812763 LOCUS DEFINITION ACCESSION VERSION

KEYWORDS

RESULT 5

g

source

FEATURES

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/note="Organ: stemach; Vector: puc18; Site 1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-181099-012-dl0&t3=1999-10-184(==1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The O.S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-159017.TV
Contact: Shaying Large Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0208
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 458)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC_library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%; Score 25; DB 10; Length 661;
100.0%; Pred. No. 2.6;
ative 0; Mismatches 0; Indels
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AZ293182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/dev scape="Adult"
/dov scape="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-181 Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence start: 5
High quality sequence stop: 636.
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RC3-ST0186-181099-012-d10 ST0186 Homo sapiens CDNA, mRNA sequence.
AW812746
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 661)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
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pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus BM487789
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/lab_host="E. coli EMDH10B**
/ note="Vectors: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; juvenile muscle 33.3%; of the final RNA pool). Single pass sequencing from 5'-end"
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BG7110.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pglln.pk008.c13 s' similar to gi|4506061 ref NP 002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1. Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gi|12737499 ref[NP_006778.2] protein kinase, AMP-activated, gamma 1
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/clone="upgm2n:pk005.j24".
/clone=lib="Normalized Chicken Breast Muscle, Leg Muscle, and EpIphyseal Growth Plate cDNA library (pgm2n)".
/kas="mala and Female".
/tissue type="Breast muscle, leg muscle and epiphyseal growth plate.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 595)
Cogburn,L.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
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/strain="Commercial broiler and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,
McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
cells
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Fax: 0064 9 373 2189
Fax: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 24; DB 17; Length 458;
100.0%; Pred. No. 6.9;
tive 0; Mismatches 0; Indels
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/clone lib="Rat Lambda ZAP Express Library"
/clone_type="vibrissae"
/cell_type="dermal papilla"
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    461
    organism="Rattus norvegicus"

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                                                                                      /lab_host="DH10B"
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Rattus norvegicus
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Gaps

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AJ396118 Akf2426 Gallus gallus cDNA clone 25f16r1, mRNA sequence.
                                                                                                                                                                               Chicken.

Gallus gallus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Avee; Neognathae; Galliformes; Phasianidae;
1 (bases 1 to 758)
Abdrakhmanov, I., Lodgin, D., Geroth, P., Arakawa, H., Law, A., Plachy, J., Korn, B. and Buerstedde, J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ926533 386 bp DNA linear GSS 21-DEC-1999
RPCI-23-256016.TJ RPCI-23 Mus musculus genomic clone RPCI-23-256016
AQ926533 .
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Judaces M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The 10stitute for Genomic Research
Tel: 301 838 0200
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 386)
                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 24; DB 9; Length 758; 100.0%; Pred. No. 7.6; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9031"
/clone="35f16r1"
/clone=1ib="dkf2426"
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
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       305 ATGCTGACCATCACTGACTTCATC 328
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AJ396118.1 GI:7127728
EST.
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GSS.
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Best Local Similarity 100.
Matches 24; Conservative
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AQ926533
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
E 1 (bases 1 to 687)
S Buerstedde Ju M.
Gallus gallus bursal lymphocyte EST
Contact: Buerstedde JM
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
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Pred. No. 7.3;
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1.4%; Score 24; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
         l (bases 1 to 636)
Burnside,J., Morgan,R.W. and Cogburn,L.A.
Chicken ESTS from a normalized liver library
Unpublished (2001)
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@UDel.Edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                             /organism="Gallus gallus"
/db xref="taxon:9031"
/clone="pglln.pk008.cl3"
/clone lib="Normalized Liver Library"
/sex="Male and Female"
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/db_xref="taxon:9031"
/clone="29a671"
/clone_lib="riken1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
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100.0%; Pred. No. '...
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AJ451523.1 GI:20261619
Phasianinae, Gallus.
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ORIGIN
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Search completed: January 6, 2003, 11:07:53 Job time : 2212.49 secs
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ORIGIN
                                               FEATURES
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CooRI; Site 2: EcoRI; Female C57BL/6J mouse kidney_and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B sites. The ligation products can be a site of the page of the page of the page of the photosis sites. The ligation products were transformed into
T1 c 104 g 89 t
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
and minmarch 12 options.
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea of Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: SP6 cow: O column: 16
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bosidae; Bovinae; Bos. 1 (bases 1 to 548)
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                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="RPCI-23-256016"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
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BI775360.1 GI:15776346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
BI775360
LOCUS
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AUTHORS
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MEDLINE
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/noce="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                          Query Match
1.3%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 20;
20, Animatches
                                                                                                                                                                                                                                                                 adrenal, and endometrium.
                                                                                                            /db_xref="taxon:9913"
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/tissue_type="pooled"
/lab_host="DH10B"

    .548
    /organism="Bos taurus"

Plate: 90 row: I column: 16
Seg primer: ATTTAGGTGACACTATAG
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                     163 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 CAGATCAAGAAGGCCTTCTTTGC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                 11 CAGATCAAGAAGGCCTTCTTTGC 33
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524, App 525, App 1, Appli 63, Appli 14, Appli 17, Appl 20, Appl 7, Appli 7, Appli 15, Appli 15, Appli 15, Appli 15, Appli 15, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19, Appli 10, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 18, Appli 19, Appli 19, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 18, Appli 18, Appli 19, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 16, Appli 16, Appli 17, Appli 18, App

Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence Sequence

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McKay, Ronald D.G.
APPLICANT: Lendahl, Urban
TITLE OF INVENTION: Newtin Expression As An Indicator
TITLE OF INVENTION: Neuroepithelial Tumors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/853,913

FLING DATE: 19920319

CLASSIFICATION: 435

PRICR APPLICATION DATA:

APPLICATION NUMBER: US 07/660,412

FILING DATE: 22-FEB-1991

PRICR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/603,803

FILING DATE: 25-60T-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/201,762

FILING DATE: 02-JUN-1988

APPLICATION NUMBER: US 07/180,548

APPLICATION NUMBER: US 07/180,548

ATTORNEY/AGENT INFORMATION:

NAME: GARANARI PATICIA

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET UNBER: 32,227

REFERENCE/DOCKET UNBER: MIT-4641AAAA

TELEPHONE: 617-861-6240

TNFORMATION FOR SEC 17 NO. 1
                                                US-09-641-638-524
US-09-641-638-525
US-09-641-638-525
US-09-61-638-1
US-09-101-146-63
US-09-101-146-63
US-09-072-384-14
US-09-072-384-14
US-08-65-259-20
US-08-65-259-20
US-08-65-259-20
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US-08-88-949-15
US-08-88-949-15
US-08-88-949-15
US-08-88-949-15
US-08-88-949-15
US-08-88-949-15
US-08-88-949-15
                                     -08-768-626-4
                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07853913
Patent No. 5338839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 11236 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Militia Dr. CITY: Lexington STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 921
1001
1001
11384
11576
11634
11743
11934
11937
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Sequence 3, A
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Sequence 15,
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Sequence 2,
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(Ggn2_6/ptodata/2/ina/5A_COMB.seq:*
(Ggn2_6/ptodata/2/ina/5B_COMB.seq:*
(Ggn2_6/ptodata/2/ina/6A_COMB.seq:*
(Ggn2_6/ptodata/2/ina/6B_COMB.seq:*
(Ggn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
(Ggn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-57-942A-2
US-08-97-252A-2
US-09-361-631-4
US-09-361-631-4
US-09-448-111D-15
US-09-448-111D-15
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US-09-342-681C-99
US-09-211-704A-1
US-09-211-704A-1
US-08-291-25-8A-1
US-08-991-25-8A-1
US-08-147-119-5
US-09-147-119-5
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US-08-396-650-2
US-08-768-626-2
US-08-396-650-3
                                                                                                                                                                                                                                                                                                                 441362 seqs, 153338381 residues
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                                                                              nucleic search, using sw model
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                                                                                                                                                                                                                                                           OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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APPLICANT: HIRANO, TOSHIO
APPLICANT: HIRANO, TOSHIO
APPLICANT: HIRANO, NISHINOMIYA
TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: D.C.
ADDRESSEE: D.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Sequence 2, Application US/08997252A Patent No. 6232453 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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Sequence 2, Application US/08537942A

Fatent No. 5753464

GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
TITLE OF INVENTION:
TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
GONESPONDENCE ADDRESSE: OBLOW, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
ADDRESSEE: P.C.
                                                                                                     Ouery Match
1.4%; Score 24; DB 1; Length 11236;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 24; Conservative 0; Mismatches 0; Indels (
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100.0%; Pred. No. 14;
Live 0; Mismatches 0; Indels
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LOCATION: 1.84
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATUE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,942A
FILING DATE: 21-NOV-1995
CLASSIFICATION UMBER: US/08/537,942A
FILING DATE: 21-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 20-MAY-1994
FILING DATE: 20-MAY-1994
FILING DATE: 20-MAY-1994
FILING DATE: 21-MAY-1993
ATPANEY/AGENT INFORMATION:
APPLICATION NUMBER: 24,618
FELEFRANCE/DOCKET NUMBER: 24,618
FELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-07-853-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1613 ACAGCACCCATCCTGACTG 1631
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MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 100.
Matches 19; Conservative
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1.1%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: sig_peptide
; LOCATION: 1..84
; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-08-997-252A-2
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 21-NOV-1995
FILING DATE: 21-NOV-1995
FILING DATE: 20-NAY-1994
PRIOR APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 20-NAY-1994
PRIOR APPLICATION NUMBER: JP 5-141178
FILING DATE: 21-NAY-1993
ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F.
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
TELECOMMUNICATION INFORMATION:
TELEFHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-517-739-2
Sequence 2, Application US/09517739
Patent No. 6307023
GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
APPLICANT: KAISHO, NISHINOMIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1613 ACAGCACCCATCCTGACTG 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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0
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            ; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PALENTIN Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6 ..
US-00-361-60-31-3/c
Sequence 3, Application US/09361631;
Patent No. 6383778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-361-631-3
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US-09-361-631-4/c
Sequence 4, Application US/09361631
Patent No. 6383778
Fatent No. 6383778
Fatent No. 6383778
FAPLICANT: Zuker, Charles S.
APPLICANT: Lindemeier, Juergen
APPLICANT: Lindemeier, Juergen
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein
TITLE OF INVENTION: Nucleic Acids Encoding Sensory Transduction
FILE REFERENCE: 023078-088720US
CURRENT APPLICATION NUMBER: US/09/361,631
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100.0%; Pred. No. 14;
tive 0; Mismatches 0; Indels
       GENE ENCODING A POLYPEPTIDE HAVING A PRE-B CELL GROWTH-SUPPORTING ABILITY
TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
                                                                                                                                                                                                                                                ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/517,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4767-0005-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/997,252
FILING DATE: 23-DEC-1997
APPLICATION NUMBER: US 08/537,942
FILING DATE: 21-NOV-1995
PRIOR APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 21-MAY-1993
ATTORNEY, AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFHONE: 703-413-3220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1613 ACAGCACCCATCCTGACTG 1631
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Matches 19; Conservative
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                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-517-739-2
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SERENTAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Lindemeier, Jon Ellion.
APPLICANT: Lindemeier, Jon Ellion.
APPLICANT: Lindemeier, Jon Ellion.
APPLICANT: Lindemeier, Jon Ellion.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic, Acids Encoding a G-Protein Coupled Receptor;
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088720US
CURRENT APPLICATION NUMBER: US/09/361,631
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/095,464
EARLIER FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 10
SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                             Gaps
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Sequence 15, Application US/08846111D
Sequence 15, Application US/08846111D
Sequence 15, Application
Sequence 15, Application
Seneral Information:
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
NUMBER OF SEQUENCES: 18
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; TYPE: DNA ORGANISM: Mus sp. ; FEATURE: FEATURE: OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4 US-09-361-631-4
                                                                                                                                                                                                                              DB 4; Length 2532;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 19; DB 4; Length 2993;
100.0%; Pred. No. 14;
live 0; Mismatches 0; Indel8
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RESULT 10
US-09-342-681C-99
; Sequence 99, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.;
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; FRIOR APPLICATION NUMBER: 60/102,279
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR PILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68, Application US/09404879A
Parent No. 6468546
GEBERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITION OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CORRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
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00.0%; Pred. No. 45;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 12;
tive 0; Mismatches
                                                                          NAME: Hanson, No. 6392016man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
                                                                                                                                            TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRRACTERISTICS:
LENGTH: 40352 base pairs
TYPE: nucleic acid
STRANDEDENSS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
         APPLICATION NUMBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATTORNEY/AGENT INFORMATION:
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100.0%; Pr.
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Best Local Similarity 100.0
Matches 19; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
Members Of The Mage-B Family and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 12;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                         STATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect For DOS 6.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,077
FILING DATE: 26-Jun-2001
CLASSIFICATION: UNKNOWN:
PRIOR APPLICATION DATA:
FILING DATE: <UNKNOWN:
                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect For DOS 6.0b
CURRENT PAPLICATION DATA.
APPLICATION NUMBER: US/08/846,111D
FILING DATE: 25-APRIL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,578
FILING DATE: 5-MAY-1996
PRIOR APPLICATION NUMBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATTORNEY/AGRAT INFORMATION:
NAME: Hanson, No. 6017705man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09443077
Patent No. 6392016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.1%; Scr
Best Local Similarity 100.0%; P.
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMINISTRATION
TELEPRONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 40352 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 GGCAGGGTGGGGAGGGGAT 486
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-846-111D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic STRANDEDNESS:
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US-09-211-704A-3/C
Sequence 3, Application US/09211704A
Patent No. 6271014
GENERAL INFORMATION:
APPLICANT: de Saint Vis, Blandine Marie
APPLICANT: Caux, Christophe
APPLICANT: Caux, Christophe
APPLICANT: Mammalian Proteinases; Related Reagents
TITLE OF INVENTION: Mammalian Proteinases; NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-211-704A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08246489
Patent No. 6225049
GENERAL INFORMATION:
APPLICANT: Lan, Michael S.
APPLICANT: Lan, Michael S.
TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED CDNA NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 18; DB 4; Length 2838; 100.0%; Pred. No. 41; ve 0; Mismatches 0; Indels
                                                                                                                         Ouery Match 1.0%; Score 18; DB 4; Length 740; Best Local Similarity 100.0%; Pred. No. 44; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A:
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 114012.012A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-850
TELEFAX: (619) 235-850
INFORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,715
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100.0%; Pre
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Matches 18; Conservative
                       LENGTH: 740
TYPE: DNA
CRGANISM: Homo sapiens
US-09-342-681C-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: IA-1
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SEQ ID NO 99
LENGTH: 740
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100.0%; Pred. No. 40;
1ve 0; Mismatches 0; Indels
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LOCATION: 3454
OTHER INFORMATION: /note= "nucleotide 3454 designated
OTHER INFORMATION: may be A or T."
                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-211-704A-1/c
; Sequence 1, Application US/09211704A
; Patent No. 6271014
; GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois
                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: SF0781K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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LENGTH: 3691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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406..2028
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NAME/KEY: CDS
LOCATION: 343..2028
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RESULT 12

467 TGGCAGGGTGGGGAGGGG 484

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Sequence 1, Application US/08991258A

Patent No. 592887

GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
ITIEE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
ITIEE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
IIP: 94111
COMPUTER: EADAR COMPATION: WORD STATES
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,258A
FILING DATE: 17-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 5769;
                                                               COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
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1.0%; Score 18; DB 1
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches
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MOLECULE TYPE: DNA (genomic)
       South San Francisco
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; LOCATION: 379..4686
US-08-652-971-1
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                             APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
TITLE OF INVENTION: and Methods
TITLE OF INVENTION: and Methods
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08652971

Batent No. 5814507

GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Genencech, Inc.
STREET: 460 Point San Bruno Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.0%; Score 18; DB 4; Length 3695; Best Local Similarity 100.0%; Pred. No. 40; Matches 18; Conservative 0; Mismatches 0; Indels
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LOCATION: 3458
OTHER INFORMATION: /note= "nucleotide 3458 designated
OTHER INFORMATION: W, may be A or T"
                                                                                                                                                                                                                                                                                                                                                                                  ZIE: 943104-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
FILOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 09-0AN-1998
ATTORNEY, AGENT INFORMATION:
NAME: Ching, Edwin P.
RECISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0781K
TELEPHONE: (650) 852-9196
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3695 base pairs
TYPE: nucleic caid
STRANDEDNESS: single
TOPOLOGY: linear
Caux, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2393 TCCTCCCCGCCCTCCCC 2376
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NAME/KEY: mat_peptide
LOCATION: 398..2032
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LOCATION: 344..2032
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                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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   APPLICANT:
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REGISTRATION NUMBER: 24.190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 781-1989
TELERAX: (415) 781-1989
TELERAX: (415) 398-3249
TELERAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
TENGTH: 5769 base pairs
TYRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 379..4686
US-08-991-258A-1
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Search completed: January 7, 2003, 20:22:10 Job time : 207.914 secs

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January 6, 2003, 16:44:13; Search time 4127.03 Seconds (without alignments) 11614.233 Million cell updates/sec
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1647
1 ttggtctgggggctggccaca.....acaccagcctcttagtcttc 1647
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2054640 seqs, 14551402878 residues
                                                                                                    OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

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2 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2 2 3 3	0,0	9	AX281579		AX28		
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17.E.4.2.9.C. 12.C. 12.C	10. 7 3. 7 3.	152129	~	AC027416		AC02		
N T 4 S 9 C 8 6 0 1 7	~ 6 4 4 ~	1722	9	AX281580		AX28		Sequence
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21008765		1867	o c	AX099774		AX09	9774	Sequence
21109876		1873	4	AF214520		AF21	4520	Sus scrof
210987	4 2.	1873	9	AX099800		AX09	0086	Sequence
21098	2.	1873	9	AX398331		AX39	8331	Sequence
510	4. c	1873	y o	AX398333		AX39	18333	Sequence
2 1 2	4 4	1873	ט פ	AX398333		AX39	8337	Seguence
7	. 2	1873	· vo	AX398339		AX39	8339	Sequence
	4 2.	2022	9	AX099804		AX09	9804	Sequence
23		8	4	AF214521		AF21	4521	Sua scrof
4. 0		777	7 (AF336381		AF33	6381	Mus muscu
າພ		901	N C	AC129703		AC12	9703	Rattus no
27		929	~	AC127107		AC12	7107	Rattus no
80	9 1.	192968	~	AC127107		AC12	7107	Rattus no
on (901	~ ;	AC129703		AC12	9703	Rattus no
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1 0		808	2 4	AX398342		SEN A	A 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	Segmence
m	; ; ;	1095	9	AX398341		AX39	8341	Sequence
34	1.	23	10	AL672140		AL6	72140	140 Mouse DNA
ın v		467	~	AC112790		ACII	2790	Mus muscu
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	human. Homo sapie	908						
200	ukaryota; ammalia;	Metazoa; Eutheria;		Chordata; Crar Primates; Cata	Craniata; Ve Catarrhini;	Vertebrata;	Eutel	leostomi; o.
AUTHORS A	Andersson,	L., Luthman, H.	hmar	, H. and Marklund, S.	und, S.			
	Variants of Patent: WO	or the h	umai 5-A	Ωųα:	d protei	ктлаве	gamma	3 subunit

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RESULT 2
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VGLYSRFDVTHLAMAQOTYNHLDMSVGRALRORTLCLEGVLSCQPHESLGEVIDRIARE
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="unnamed protein product"
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ive 0; Mismatches
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EPPGGGEGRERSTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDDWSLATEFPATESTGLEATFFRYTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDWSLATEFPATEAWECELEGLLEERPALCLSPQAFFFRLGWDDELRKPGAQIYM
RFWQEHTCYDAMATSKLVIPDTMLETKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDF1LVLHRYTRSPLVQIYETEQMK.ETWREIYLQCFKPLVSISPNDSLFEAVYTLI
AVNIHTRLPUDPVSGNVLHITHKRKLLKFHHFFSLLDRSFLYRTLGDGGGGTFRDL
AVVLETAPILTALDIFYDRRYGALPVNNECGQVVGIYSRFDYTHLAQQYTNHLDMSV
GEALRQRTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
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                     Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2115)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Roge!-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                              Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof Parent: WO 0120003+A 29 22-MAR-2001;
PRETITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Brnst (DE)
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/db_xref="G1:13538837"
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/organism="Homo sapiens"
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AF214519
2115 bp mRNA linear PRI 03-JUN-2000 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 2115)
Milan, D., Jeon, T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H.,
Lundarrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
Science 288 (5469), 1248-1251 (2000)
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2 (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,

Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,

Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.

Direct Submission

Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish

University of Agricultural Sciences, BMC box 597, Uppsala 751 24,

Sweden
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/db_xref="tunamed protein product"

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/codon_start=1

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TQHLGVVSLSDILQALVLSPAGIDALGA"

TQHLGVVSLSDILQALVLSPAGIDALGA"
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Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
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Batent: WO 0120003-A 3 22-MAR-2001;
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Pred. No. 0;
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Sequence 3 from Patent WO0120003.
AX099776.1 GI:13538810
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Mammalia; Eutheria; Primates;
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QCHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEKI"
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                                                 Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 2290)

Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit Biochem. and their role in AMP binding

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Submitted (12-OCT-1999) Carling D., Cellular Stress Group,
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road
London, W12 ONW, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /gene="AMPK gamma 3"
/function="AMP-activated protein kinase regulatory
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Organism="Homo sapiens"
/db_xref="taxon:9606"
22. .1500
/gene="AMPK gamma 3"
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Carling, D.
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restriction digest.
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  1441 TCAGGCACTGGTGCTCAGCCCTGCTGGCATGCCCTCGGGGCCTGAGAAGATCTGAG 1500
               1501 TCCTCAATCCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAAACTCAGC 1560
                                                            1502 TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAATGAAGGGAACTGGAGAACTCAGC 1561
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Variants of the human amp-activated protein kinase gamma 3
Patent: WO 0177305-A 2 18-OCT-2001;
Arexis AB (SE)
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Pred. No. 1.6e-204;
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100.0%; Pred. No. ...
0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
306 c 286 g 166
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Seguence 2 from Patent WO0177305.
AX281579
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PRI 09-JAN-2002

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Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
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Submitted (108.5EP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
# (Dasses I to 206854)
Waterston, R.H.
Direct Submission
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206854)
Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. L.
MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
AC009974
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Contact: Summary Statistics
Center project name: H_NH0459119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 206854)
Harris,A. and Cotton,M.
The sequence of Homo sapiens BAC clone RP11-459119
1 (bases 1 to 206854)
Waterston,R.H.
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Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (03-JAN-2002) Genome
University School of Medicine,
MO 61108, USA
6 (bases 1 to 206854)
                                                                           AC009974.9 GI:16799058
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Waterston, R.H.
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Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://www.resgen.com) or Pieter de Jong (http://www.resgen.com) or Pieter de Jong (http://bappac.med.buffalo.edu)
WECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-1077K22; the clone sequenced to the left is RPI1-64705. Actual start of this clone is at base position 1 of RPI1-459I19; actual end is at base
                                                                                                                                                                                                                                                                                            Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.
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hote="match to EST AI670836 (NID:94850567) wa04910.x1"
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/note="match to EST AL567345 (NID:g12920610)"
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/note="match to EST BG477625 (NID:g13409904)"
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note="match to EST BE314060 (NID:g9134719)"
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/note="match to EST B1059713 (NID:g14467240)"
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(NID:914565249)"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168406 CACACCCTTGGCTCAAGCTGATCCTGCCGGGGTGGGCACTCCACCAACAGGGTGGGATG 168347
                                                                                                                   (NID:91521226) zk53e10.rl"
                                                                                                                                                                                                                             to EST AA043371 (NID:g1521226) zk53e10.rl"
                                                                                                                                                                                                                                                                  note="match to EST A1670836 (NID:g4850567) wa04g10.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 168286 CACGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTGAGCCTGCTGGAAGGCGTGCTGGAAGAGAG 168227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="match to EST BE047599 (NID:98364652) tz39c01.y1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI860958 (NID:95514574) wl56f05.xl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match to EST AA481361 (NID:g2210913) zv44e01.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NID:94740791) tt54b06.x1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AGGICCCCGGTCCAGGCCAGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAGAC 306
                                                                                                                                                  note="match to EST T64073 (NID:g667938) yc05d12.r1"
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                                                                                                                                                                                         to EST BI059713 (NID:g14467240)"
                                                                                                                                                                                                                                                                                                                                             /note="match to EST BE908408 (NID:g10402954)"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to EST BF304755 (NID:g11251653)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match to EST BG470047 (NID:913402322)"
                                                                                                                                                                                                                                                                                                                                                                                        (NID:g11061273)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="match to EST BG477625 (NID:g13409904)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match to EST AL567345 (NID:912920610)"
17. .1084
                                                                           'note="match to EST BG470047 (NID:913402322)
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                note="similar to Homo sapiens EST BI114348
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(NID:g14565249)"
967. 1085
                                                                                               complement (557, .558)
note="match to EST AA043371
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/note="match to EST
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/note="match
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Best Local Similarity 99.8
Matches 405; Conservative
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Bitten, B. Linton, L. Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgaler, B., Brown, A., Beda, F., Boukhgaler, B., Brown, A., Beda, F., Colangelo, M., Colline, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dear, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand-Pierre, N., Grant, G., Gyrette, M., Grand, J., Grant, G., Gyrette, M., Grann, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Krein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McGurk, A., McKernan, K., McPheeters, R., Maldrim, J., Meneus, L., Mihova, T., Minova, T., O'Donnell, P., O'Neil, D., Olivar, T., M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stange, Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vonny, G. Zainoun, J., Zimmer, A. and Zody, M., Kwan, D., Ye, W. J., Vonny, G. Zainoun, J., Zimmer, A. and Zody, M., Wison, B., Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Submitsed on Jun 7, 2000 this sequence version replaced gi:7342115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker:
Genter: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Center project name: 17458
Center clone name: 504 G 11
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 143264 bases at least Q40
Consensus quality: 145503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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f 1097 bp in length
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contig of 1297 bp in length
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contig of 1321 bp in length
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of 1041 bp in length
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contig of 1286 bp in length
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                   1 (bases 1 to 152129)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-504G11
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3924 5020: cont
5021 5120: gap of
5121 6161: cont
6162 6261: gap of
6262 7547: cont
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be preserved.
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                                    Db 168226 GCCTGCCCTGTCCCCGCA-GCCCCAAGCTGGGCTGGGATGACGAACT 168168
                                                                                                                          Db 168167 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGAGACACACCTGCTACGATGC 168108
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AC027416.2 GI:8317289
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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         GCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCAAGCTGGGCTGGGATGACGAACT
                                                                                                 547 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGC
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                                                                                                                                                                                                                 Db 168107 CATGGCAACTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAG 168062
                                                                                                                                                                                                                                                                                                                                                                  linear
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100.0%; Pred. No. 2.7e-136;
:ive 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
325 c 271 g 226
                                                                                                                                                                                                                                                                                                                                                        Sequence 4 from Patent WO0177305.
AX281581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            AX281581.1 GI:16608832
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      GAAGATCTGAGTCCTCAAGCCACCTGCACCTGGAAGCCAATGAAGGAACTG
      1549

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      GAAGATCTGAGTCCTCAATCCAAGCCACCTGCACCTGGAAGCCAATGAAGGAACTG
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Db 139898 GAGAACTCAGCCTTCATCTTCCCCCACCCCCATTTGCTGGTTCAGCTATGATTCAGGTAG 139957
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16.9%; Score 278; DB 2; Length 15
Best Local Similarity 100.0%; Pred. No. 9.2e-137;
Matches 278; Conservative 0; Mismatches 0; Indels
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22029. .24319
note="assembly_fragment"
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0271. .33968
note="assembly_fragment"
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note="assembly_fragment"
1386. .55871
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5972, .60595
note="assembly_fragment"
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hote="assembly_fragment"
6696. .73218
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note="assembly_fragment"
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RESULT 10 AC027416/c

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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boukhgalter, B., Brown, A., Barten, W., Bada, F.,
Baddwin, J., Barna, N., Bastien, V., Beda, F.,
Baddwin, J., Barna, N., Bastien, V., Beda, F.,
Baddwin, J., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Cascle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Klein, J., LaRocque, K., Landers, T., Lehoczky, J.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Murphy, T., Naylor, J., Mihova, T., Miranda, C., Morrow, J.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Direct Submission

Loudy, G., Zainoun, J., Zimmer, A. and Zody, M.,
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker:
AC027416 152129 bp DNA linear HTG 07-JUN-2000
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: M13 M77861
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 143376 bases at least Q40
Consensus quality: 145264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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------ Project Information
Center project name: L7458
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-504G11
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                              HTG; HTGS PHASEI; HTGS DRAFT.
Homo sapiens.
Homo sapiens
                                                                                                                                               AC027416.2 GI:8317289
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6162 6261: gap of 100 bp 6262 7547: contig of 1286 bp in length 7648 9983: contig of 2336 bp in length 10084 10083: gap of 100 bp 100 bp 10084 12557 12665: gap of 100 bp 12657 15643: contig of 2387 bp in length 1255 12659: contig of 2387 bp in length 12657 15643: contig of 2387 bp in length
                              100 bp
of 1321 bp in length
100 bp
of 1097 bp in length
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113191 123496: contig of 10306 bp in length
123497 123596: gap of 100 bp
123597 137837: contig of 14241 bp in length
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1724 19466: contig of 2243 bp in length
19467 19566: gap of 100 bp
19567 21928: contig of 2362 bp in length
21929 22028: gap of 100 bp
22029 24319: contig of 2291 bp in length
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contig of 1297 bp in length
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6161: contig of 1041 bp in length
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66595: contig of 5900 bp in length
6695: gap of 100 bp
73218: contig of 6523 bp in length
77118: contig of 3797 bp in length
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contig of 2640 bp in length
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30170: contig of 3011 bp in length
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clone lib="RPCI-11 Human Male BAC"
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2503, .3823
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/db_xref="taxon:9606"
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137838 137937; gap of
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PAT 03-NOV-2001
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                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Robic, A., Jeon, J.-T., Rey, V., Amarger, V., Chardon, P., Looft, C., Andersson, L., Gellin, J. and Milan, D.

Construction of a high-resolution RH map of human 2q35 region on TNG panel and comparison with physical map of porcine homologous Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1082 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACACCACCCATCCTGACTGCACTGGACTTC 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1022 GGTTCCCTGCTGCCCCGGCCCTCCTTCCTACCGCACTATCCAAGATTTGGGCATCGGC 1081
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Genetique Cellulaire
Institut National de Recherche agronomique (INRA)
BP27, 31326 Castanet Tolosan, France
Tel: (33) 5 61 28 53 08
Email: arobic@roulouse.inra.fr
Primer A: TGGGCATGGGCACATTCC
Primer B: GACCACAGGCACATTCC
Primer B: GACCACAGGCACATTCC
Primer B: GACCACAGGCACATTCC
Initial incubation: 94 degrees C for 4 min
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10.2%; Score 168; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.1e-77;
Matches 168; Conservative 0; Mismatches 0;
                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                 363 t
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
504 c 534 q 363
                                                                                   Sequence 3 from Patent WO0177305.
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               534 g
                                                                                                                                    AX281580.1 GI:16608831
      Db 37999 TCGACACCATGCTGGAG 37983
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G67375.1 GI:11841655
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Best Local Similarity
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                                                                                                                                                                    human.
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ORIGIN
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AUTHORS
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                                                     RESULT 11
AX281580
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G67375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AGTGTGAGCTAGAAGGCCTGCTGGAAGAGAGCCTGCCCTGTGCCTGTCCCCGGCAGGCCC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 CATITICCCAAGCTGGGCTGGGATGACGAACTGCGGAAACCCGGCGCCCAGAICTACATGC 575
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12.0%; Score 197; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.4e-93;
Matches 197; Conservative 0; Mismatches 0;
                                                                                          /note="assembly_fragment"
42467. 46365
/note="assembly_fragment"
46466. 51285
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51386. 55871
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/note="assembly_fragment"
60696. .65595
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66696. .73218
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7648. .9983
                            5121. .6161
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101294. 113090 /note="assembly_fragment"
               note="assembly_fragment'
                                                                                                                                                                       'note="assembly_fragment"
.5144. .17123
                                                                                                                                                                                                                                                                                      19567.<sup>-</sup>.21928
/note="assembly_fragment"
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24420. .27059
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!7160. .30170
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38280. 42366
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77216. .85022
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19567. .21928
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misc_feature
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/codon start=1
/protein id="CAC35798.1"
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ISPNDSLFRAVYALIKNRIHELPULDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
ISPNDSLFRAVVVLETAPILTALDIFVDRRVSALPVNETGQVVGLYSRFDVI
HLAAQQTYNHLDMNVGEALRQFTCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE
TQHLGGVVSLSDILQALVLSPAGIDALGA"

583 c 529 g 375 t
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AF214520
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                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

    (bases 1 to 1867)

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1 (bases I to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kälm, E., Roy, P.L., Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Reinsch, N., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                    Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof same, and uses thereof batent: WO 0120003-A i 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                               Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., 1e Roy, P. and
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 2.7%; Score 44; DB 6; Length 1867;
Local Similarity 100.0%; Pred. No. 1.3e-11;
nes 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629 GTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529 GTCATCTTCGACACCATGCTGGAGATCAAGAAGGCCTTCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
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Science 288 (5469), 1248-1251 (2000)
                     Sequence 1 from Patent WO0120003.
                                                                                                                                                                                                                                                                                                                                                     1. 1867
/organism="Sus scrofa"
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472. 1389
                                                      AX099774.1 GI:13538808
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                                                                                                             scrofa
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Sus scrofa
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AF214520
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                     Primers were defined on sequence AA178898 (cDNA). No intron.
Location/Qualifiers
1. .106
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Denaturation: 94 degrees C for 30 seconds
Annealing: 55 degrees C for 30 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 33
Thermal cycler: Perkin Elmer 9600
Protocol:
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100.0%; Pred. No. 2.9e-18;
Live 0; Mismatches 0;
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100.0%; Pred. No. 8.6e-16;
iive 0; Mismatches 0;
                                                                                                             Template: 25 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: 0.1 units/reaction
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| Chromosome="15" |
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Search completed: January 7, 2003, 20:19:51 Job time: 4648.03 secs

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/label= "T559C"
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Human immune/haema
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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ABA4106
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                                                                                         Marklund
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                                    06-APR-2001; 2001WO-SE00765
                                                    07-APR-2000; 2000US-195665P
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Matches 1647; Conservative
                                                                                      Andersson L, Luthman
                                                                                                        2001-657170/75
                                                                     (AREX-) AREXIS AB.
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP) -activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as dispetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK carbotity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. Primers that can detect greeferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered alleie of PRKAG3 or a
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                                                                                                                                                                                                                                                                            Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                 monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
(KALM/) KALM E.
                                                             Location/Qualifiers
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heterotrimeric AMPK consisting of PRKAG3 or its mutant, are usefu screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gen in a sequence encoding the first cystathione beta synthase (CBS) of PRKAG3 and is useful in gene therapy.
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Pred. No. 0;
0; Mismatches
                                                                                                 83.3%;
99.9%;
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Best Local Similarity 99.9
Matches 1422; Conservative
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(ANDE/) ANDERSSON L.
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The present sequence is a cDNA encoding human adenosine monophosphate CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRKAG3 is a carbohydrate metabolism, particularly in skeletal muscle. PRRKAG3 is as diabetes, obesity, and disorders associated with muscle metabolism cc as diabetes, obesity, and disorders associated with muscle metabolism cc activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic consultation, genetic testing and prognosis of a metabolic disorder. Preferably a carbohydrate metabolism disorder. Primers that can detect to preferably a carbohydrate merabolism disorder. Primers that can detect of a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered altele of PRKAG3 or a screening compounds able to modulate AMPK acrivity. Nucleic acid servening compounds able to modulate AMPK acrivity. Nucleic acid na sequence encoding PRKAG3 and is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain
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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAH43681-84 represents genomic fragments encoding the human AWP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P11A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the substitution of a T for a C at nucleotide 1037, resulting in the substitution of a T for a C at nucleotide loss.
                                                Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma, archritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiatthmatic; antiatthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                      426
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719
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                                                                                                                                                                                                                                                                CACGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTGAGAGGCTAGAAGGCCTGCTGCTGGAAGAGG
                                                                                                                             780 GCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTCCCCAAGCTGGGCTGGGATGACGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGC
                                                                                               CCTCCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGC
                                                                                                                                                                                                                         CACGGAGTTCCCAGCCACAGAGGCCTGGGAGTGTGAGAGGCTAGAAGGCCTGCTGGAAGAGAG
                                                                                                                                                                                                                                                                                                                                                  GCCTGCCCTGTGCCTGTCCCCGCAGGCCCCATTTCCCCAAGCTGGGGATGACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840 GCGGAAACCCGGCGCCCAGATCTACATGCGCTTCATGCAGGAGCACCTGCTACGATGC
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2000US-0560875
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27-APR-2000;
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cc sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; seem cell growth factor activity; differentiation activities; seem cell growth factor activity; immunomodulatory activity; itseus growth activity; confincion or chemokinetic activities; haemostatic or may be invention activities; receptor or ligand activities; or may be invention activities; receptor or ligand activities; or may be invention are useful for preventing, treating or ameliorating medical confittons, e.g., by protein or gene therapy. Such conditions include the invention are useful for preventing, treating or anticions include cancers, haematopoletic disporders (e.g., myeloid or lymphoid cell disporders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disporders (e.g., osteoporosis), and abnormal vacual growth. Polypeptides involved with tissue regeneration and forgal infections and ulcers), while those with the alling (e.g., of burns, incisions and ulcers), while those with growth. Polypeptides and molypeptides may be used in cell culture to give rise to neuroepinelal colls encoding the plannand or ventivity may be used in cell culture to give rise to neuroepinelal colls commended to anoment or remained by anoment or remained to remember to represent the colls commended to anoment or remained to remember or mental and proper independent or promote cell that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypoptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

ö 24.2%; Score 398; DB 22; Length 547; 100.0%; Pred. No. 2.5e-181; Indels Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other; 100.0%; Pred. Best Local Similarity 100. Matches 398; Conservative Query Match

771 ATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAACATAAGATTGAGA 830

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Gaps

CCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCTCCTTCTCTCCTAATG 153 CCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGGTCTCCATCTCCTAATG 890 93 ATAGCCTGTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGCCTGCTTC 154 831 94 891 원 ò g g ò

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TGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTG 101 274 334 g ò ద

1130

393

RESULT 6

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Length 1014; Indela CAGGTACACAGGCTGGTGCTAGTGGACGAGCCCAGCATCTCTTGGGCGTGGTCTCCCTC 1429

16.9%; Score 278; DB 22; I larity 100.0%; Pred. No. 1.5e-123; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 278; Conserv

1370

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1490 857 1550

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| TCCGACATCCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGA 1489

GAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACCTGGAAGCCAATGAAGGGAACTG GAGAACTCAGCCTTCATCTTCCCCCCACCCCCATTTGCTGGTTCAGCTATGATTCAGGTAG

916

917 GAGAACTCAGCCTTCATCTTCCCCCACCCCCATTGCTGGTTCAGCTATGATTCAGGTAG 976

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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                               Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                                    /number = "Intron 10"
/note= "3' portion of intron 10"
12..79
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r≈ "Intron 11"
                                                                                                                                                                                                                                                                                                                                                 Marklund S;
                                                                                                                                                                                                                       "Intron 12"
                                                                                                      Location/Qualifiers
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/number= "Exon 13"
857..1014
                                                                                                                                                       'number= "Exon 11"
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       AAH43684 standard; DNA; 1014 BP
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/*tag= d
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/*tag= e
                                                   PRKAG3 intron 10 - 3'UTR.
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                                                                                       sapiens
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                                    21-JAN-2002
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                      AAH43684;
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27552.
                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
               AAK72740 standard; DNA; 3425 BP
                                                                                                                                                                                                               2000US-0186350
2000US-0189874
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2000US-0198123
2000US-0205515
2000US-0205467
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2000US-0215135
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2000US-0220963.
2000US-0220964.
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2000US-0180628.
2000US-0184664.
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2000US-0216880.
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2000US-0217496.
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2000US-0225266.
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2000US-0225447.
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                                                   (first entry)
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14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
                                                                                                                 Homo sapiens.
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
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02-MAR-2000;
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17-MAR-2000;
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07-JUN-2000;
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                                                   06-NOV-2001
                                 AAK72740;
RESULT
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The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3D DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A, in exon 4 variation may be a substitution of a Use in condition of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1377, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the in intron 6.

Sequence 1014 BP; 192 A; 325 C; 271 G; 226 T; 0 other;

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2000US-0226681.
2000US-0226868.
2000US-0227182.
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2000US-0232080.
2000US-0232081.
2000US-0232397.
2000US-0232397.
2000US-0232399.
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2000US-0233063.
2000US-0233064.
2000US-0233065.
2000US-0234223.
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2000US-0235834.
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2000US-0239935.
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2000US-0241221.
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2000US-0241786.
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2000US-0229345.
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2000US-0231244.
2000US-0231413.
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14-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
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23-AUG-2000;
23-AUG-2000;
23-AUG-2000;
21-SEP-2000;
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29.5EP-2000;
29.5EP-2000;
02-0CT-2000;
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25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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08-NOV-2000; 2000US-0246609.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249201.
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17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-025198.
05-DEC-2000; 2000US-0251988. 05-DEC-2000; 2000US-025031. 05-DEC-2000; 2000US-0251988. 05-DEC-2000; 2000US-0251988. 06-DEC-2000; 2000US-0251856. 08-DEC-2000; 2000US-0251868. 08-DEC-2000; 2000US-0251869. 08-DEC-2000; 2000US-0251869. 08-DEC-2000; 2000US-0251990. 11-DEC-2000; 2000US-0251990. 11-DEC-2000; 2000US-0251990.

(HUMA-) HUMAN GENOME SCI INC

Barash SC, Ruben SM Rosen CA,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 27552; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
cupplement the patients own production of (1). Additionally, (1)
polymuclectides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polymuclectides may be used to prevent,
cancers and cancer immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAKS4942 to AAKS4950 and AAM82169 represent sequences used in the exemplification of the present invention

Sequence 3425 BP; 916 A; 794 C; 951 G; 764 T; 0 other;

ö Query Match 15.3%; Score 252; DB 22; Length 3425; Best Local Similarity 100.0%; Pred. No. 5.1e-111; Matches 252; Conservative 0; Mismatches 0; Indels 0,

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Gaps

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2000US-0229345.
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2000US-0229509.
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                                       2000US-0227182.
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2000US-0246609.
2000US-0246610.
2000US-0246611.
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       2000US-0226681
   22-AUG-2000;
22-AUG-2000;
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30-AUG-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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29.5EP-2000;
29.5EP-2000;
29.5EP-2000;
20.0CT-2000;
20.0C
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14-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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     CAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGAGAGATCTGAGTCCTCAATCCCAAGC 1515
CGAGACCCAGCATCTTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGGTGCT 1455
                                                                                                                                         CACCTGCACACCTGGAAGCCAATGAAGCGAACTCGGAACTCAGCCTTCATCTTCCCCCA 1575
                                                                                                                                                                                                                CCCCCATTIGCTGGTTCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGC 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27553
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ID AAK72741 standard; DNA; 3425 BP
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2000US-018664.
2000US-018664.
2000US-018974.
2000US-0199076.
2000US-0199076.
2000US-02515.
2000US-0215135.
2000US-022514.
2000US-0225214.
2000US-0225214.
2000US-0225214.
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2000US-0225758.
2000US-0225759.
2000US-0226279.
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                                                                                                                                                                                                                                                                                     WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 - JAN - 2000; 24 - FEB - 2000; 26 - FEB - 2000; 27 - FEB - 2000; 28 - JUN - 2000; 28 - JUN - 2000; 28 - JUN - 2000; 29 - JUN - 2000; 20 - J
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us-09-826-581-5.oligo.rng

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1576 CCCCCATTTGCTGGTTCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGC
         1456 CAGCCCTGCTGGCATCGATGCCCTCGGGGCCTGAGAAGATCTGAGTCCTCAATCCCAAGC
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                                                                                                                                                3245 CCCCCATTGCTGGTTCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGC
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
c activity, and can be used in gene therapy and vaccine production. (I)
c proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
c example, they may be used to treat disorders associated with decreased
c expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent.
C diagnose and treat immune/haematopoietic-derived cells. AAK64703
c cancers and cancer metastasses of haematopoietic-daried genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54922 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 27553; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.3%; Score 252; DB 22; Length 3425; 100.0%; Pred. No. 5.1e-111; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3425 BP; 916 A; 794 C; 951 G; 764 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM;
                                                2000US-0249210.
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                                 2000US-0249209
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Best Local Similarity 100.(
Matches 252; Conservative
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17-NOV-2000;
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17-NOV-2000;
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Human; AMP-activated protein kinase gamma 3 subunit, PRKAG3; variant,
metabolic disease; diabetes; obesity; substitution; ds.
                                                                                                       '*tag= a
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/*tag= c
/number= "Intron 5"
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number= "Intron 9"
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AAH43683 standard; DNA; 1722 BP.
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/number= "Exon 6
612..736
                                         PRKAG3 intron 4 - intron 10
                                                                                                                            14..95
/*tag= b
                            (first entry)
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987..1041
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                            21-JAN-2002
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1583 ACATTCCGAGACTTGGCTGTGGTGCTGCAGACACCCATCCTGACTGCACTGGACATC 1642
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disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168; DB 22; Length 1722;
Pred. No. 1.5e-70;
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 /note= "5' portion of intron 10"
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                                                                                            06-APR-2001; 2001WO-SE00765
                                                                                                                             07-APR-2000; 2000US-195665P
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                                                                                                                                                                                             Luthman
                                                                                                                                                                                                                          WPI; 2001-657170/75.
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                              WO200177305-A2
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                                                                                                                                                                                           Andersson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in intron 6.
                                                                18-OCT-2001
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label contact of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents at greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tas microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the operation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                         New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.2%; Score 85; DB 22; Best Local Similarity 100.0%; Pred. No. 1.4e-30 Matches 85; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                    Chen W, Rank DR;
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                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   711 ACAGCAAGAAGCAGAGCTTTGTGGG
                                                                            26-MAY-2000, 2000US-0207456.
30-UJM-2000; 2000US-060408.
30-AUG-2000, 2000US-0632366.
21-SEP-2000; 2000US-0234587.
27-SEP-2000; 2000US-0236359.
                    30-JAN-2001; 2001WO-US00662
                                                          2000US-0180312
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ABA55162 standard; DNA; 378
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                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                     WPI; 2001-496933/54.
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                                                                                                                                                                    04-OCT-2000;
                                                          04-FEB-2000;
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and nongenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 5.2%; Score 85; DB 22; Length 378; Local Similarity 100.0%; Pred. No. 1.4e-30; hes 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe SEQ ID NO: 3414.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                            Claim 1; SEQ ID No 3373; 530pp; English.
                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 ACAGCAAGAAGCAGAGCTTTGTGGG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 ACAGCAAGAAGCAGAGCTTTGTGGG 735
                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK03423 standard; DNA; 378 BP
                                                                                                        Chen W,
 03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                              04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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2000US-0234687.
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2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                        Penn SG, Hanzel DK,
                                                                                                                                    WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
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                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #3373 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene expression, heart, microarray, vascular system; probe, cardiovascular disease, hypertension; cardiac arrhythmia,
                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 378;
                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 ACAGCAAGAAGCAGAGCTTTGTGGG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 ACAGCAAGAAGCAGAGCTTTGTGGG 267
                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA24907 standard; DNA; 378 BP
                                                                                                  03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     congenital heart disease; ss
                            30-JAN-2001; 2001WO-US00669
                                                                                    2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                       WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157274-A2.
                                                                                      30-JUN-2000;
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09-AUG-2001
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Gaps

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Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                          12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                    AAI13465;
                                                                                                                                Query Match
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                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                          351 AGATCAAGAAGGCCTTCTTTGCTCGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG 292
                                                                                                                                                                                                                                                                                                       651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG 710
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
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                                                                                                                 Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human bone marrow expressed single exon probe SEQ ID NO: 3431
                                                                                                                                                                                                                                                            Length 378;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                    Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                           DB 22; 1
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                                    DR;
                                    Rank
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            MOLECULAR DYNAMICS INC
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                                   Chen W,
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                 85; Conservative
                                   Hanzel DK,
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                                                      WPI; 2001-483446/52
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 85; Conserv
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27-SEP-2000;
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                                                                                                                                                                                                              invention.
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                                  Penn SG,
            (MOLE-)
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

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               probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #3398 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                    651 AGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGCCCCTCTATGGG 710
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; microarray; gene expression; cervical epithelial cell;
The present invention provides a number of single exon nucleic acid
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                                                                                                                                                      Length 378;
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                                                                                                               Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                    DB 22; 1
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                                                                                                                                               Claim 25; SEQ ID No 3398; 487pp; English
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                                                                                                                                                                                                                                                                                                        291 ACAGCAAGAAGCAGAGCTTTGTGGG 267
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2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                   the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer; ss.
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                                                                                                                                                                Best Local Similarity
Matches 85; Conserv
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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us-09-826-581-5.oligo.rng

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CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: January 6, 2003, 09:56:02 Job time : 329.832 secs

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score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size

Searched:

Database :

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AMI/BBYB
2D38d10.rl Stratagene muscle 937209 Homo sapiens CDNA clone
IMAGE:611731 5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNĀ sequence.
                                                             BF601364 266320 MA
BR49018 PM2-ET020
BM49018 pgp2n-pk0
BI555697 603239764
BH22415 UI-M-BH2-ET020
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BF510369 MB-P-AY1-BF99510 MR2-GN015
BF634609 BB634609 BB634609
BB628677 BB629521
BB629521 BB629521
BB629531 BB629521
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AZ745562 RPCT-L24-1
AZ745562 RPCT-L41
AZ74562 RPCT-L41
AZ74562 RPCT-L41
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AIT7537 EBS612.y
AG693634 HS 5456
BA562894 VA44A10.F
BF76104 G03053090
BE7761793 G03395042
                          BM487789 pgm2n.pk0
BG713637 pglln.pk0
AJ451523 AJ451523
AJ396118 AJ396118
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1 (bases 1 to 413)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizhan,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wathe,Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                        AL519471 AL519471
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1280 Std Error: 0.00
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444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                        AQ431286
BB634609
BB628877
BI775360
AW314499
BE126712
BG713637
AJ451523
AJ396118
BF601364
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BB527609
AW122415
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BI134322
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DEFINITION
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VERSION
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JOURNAL
COMMENT
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BI344527 373008 MA
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AW427435 63185 MAR
BF890374 291826 MA
                                                           ; Search time 2107.51 Seconds (without alignments) 12656.598 Million cell updates/sec
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     GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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Score

Result Š. 164 68 42 41 41

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/clone="IMAGE:358890"
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Best Local Similarity 99.2%;
Matches 118; Conservative (
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Sus scrofa
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BI344527
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                                                Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1. (bases 1 to 485)
1. (bases 1 to 485)
1. (bases 1 to 485)
1. Hillier; L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Trewaskis, E., Waterston, The Washu-Merck EST Project
1. Unpublished (1995)
1. Contact: Wilson RK
1. Washington University School of Medicine
1. Vat 286 1800
1. Fax: 314 286 1800
1. Fax: 314 286 1800
1. Fax: 314 286 1810
1. Email: est@watson.wustl.edu
1. This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
1. Insert Length: 775 Std Error: 0.00
1. Seq primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W94830 485 bp mRNA linear EST 29-NOV-1996 zel3el0.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone MAGE:358890 5', mRNA sequence.
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100.0%; Pred. No. 4.9e-65;
iive 0; Mismatches 0;
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.
Location/Qualifiers
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/db_xref="GDB:1275434"
/db_xref="taxon:9606"
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Matches 164; Conservative
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Best Local Similarity
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W94830
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68913-0166, USA
Tal: 402 762 4366
Fax: 402 762 4390
Email: smithGemail:marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
pCR PRIMERS
FOR PRIMERS
FORMARD: AGGAAACAGCTATGACCAT
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(Dases I to 572)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Design and use of two pooled tissue normalized cDNA libraries for Chipublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon_9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab host="DH108"
/note="Vector: pCMV_SPORT6; Site_1: Not1; Site_2: Sal1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1488 GAGAAGATCTGAGTCCTCAATCCCAAGCCACCTGCACCTGGAAGCCAATGAAGGGAAC 1547
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                                                                                                                                                                                                                                                                                                                                                                                         Length 485;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 14; Length 48
Pred. No. 1.9e-20;
0; Mismatches 1; Indels
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                             112 t
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Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG.
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BASE COUNT ORIGIN

LOCUS DEFINITION ACCESSION

VERSION

RESULT 4 AW356079

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KEYWORDS SOURCE ORGANISM

AUTHORS

MEDLINE JOURNAL

COMMENT

TITLE

REFERENCE

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Single pass sequencing. Bases called and trimmed with phred v0.889094. A Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                         EST 25-APR-2001
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
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/note="Vector: pCWV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 444)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                       AW427435 422 bp mRNA linear 63185 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE: 402 762 4366
Fax: 402 762 4390
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6.4e-08;
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100.0%; Pred. No. v...
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/db_xref="taxon:9913"
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Plate: 32 row: F column: 22
Seg primer: ATTTAGGTGACACTATAG.
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DEFINITION
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ORGANISM
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MEDLINE
COMMENT
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                                                                                                  ACCESSION
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    RESULT 5
AW427435
                                                                                                                                           KEYWORDS
SOURCE
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BF890374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Figure 1. Smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
V0.9809044. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                          EST 25-APR-2001
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libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                   Gaps
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Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta. 190 c 151 g 124 t 1 others
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                                                                                                                     Length 572;
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38073 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
AW356079
                                                                                                                                                                0; Indels
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                                                                                                                                                                                                       1247 TACAACCACCTGGACATGAGTGTGGGGAGAGCCCTGAGGCAG 1288
                                                                                                                                                                                                                                 409 TACAACCACCTGGACATGAGTGTGGGGAGAAGCCCTGAGGCCAG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAG 304
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                                                                                                                   Score 42; DB 13; I
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 41; DB 10; 100.0%; Pred. No. 6.3e-08; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 t
                                                                                                                                                                0; Mismatches
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/clone_lib="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 17 row: P column: 9
Seg primer: ATTTAGGGTGACACTATAG.
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                                                                                                                Query Match 2.6%; is Best Local Similarity 100.0%; Matches 42; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Conservative
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Best Local Similarity
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Gape

source

FEATURES

BASE COUNT

ORIGIN

Matches

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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS FORWARD: AGGAAACAGCATGACCAT BACKWARD: GTTTTCCAGTCAGCAGC BACKWARD: GTTTTCCAGTCAGCAGC Seq primer: 1 column: 16 Seq primer: ATTTAGGTGACAGTAAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus Burdatus (Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos 1 (bases I to 298) Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heacon, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Reele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
PCR PRIMERS
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                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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AW314499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCCAAG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTCCCCAAG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 13; I
Pred. No. 6.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.5%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 6.8 Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               adrenal, and endometrium
                                                                                                                                                                                                                                                                       db_xref="taxon:9913"
/clone_lib="MARC_2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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/clone_lib="MARC_3BOV"
/tissue_type="pooled"
                                                                                                                                                                                                                                                     organism="Bos taurus"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 11 row: H column: 23
Seq primer: ATTTAGGGTGACACTATAG.
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ACCESSION
VERSION
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SOURCE
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                                                                                                                                                                                                                                                                                                             Fax: 402 702 4350
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS: AGGAAACAGCTATGACCAT
BACKWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGG
Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACATATAG.
Casas, E., Wzay, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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1 (bases I to 540)

Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, C. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21180013
Contact: Smith TPL
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 763 4390
Email: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5%; Score 41; DB 12; I
:00.0%; Pred. No. 6.5e-08;
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/clone_lib="MARC 3BOV"
/rissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
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Best Local Similarity
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146 ATGCTGACCATCACTGACTTCATC 169
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BM487789.1 GI:18608720
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BG713637
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            /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle = 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 461)
Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P., McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D. Expressed sequence tags of cDNA clones from rat dermal papilla
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                                                                                                                                     2.2%; Score 37; DB 10; Length 298; 100.0%; Pred. No. 4.2e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:10116"
/clone lib="Rat Lambda ZAP Express Library"
/tissue_type="vibrissae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 24; DB 10; Length 461;
100.0%; Pred. No. 5.1;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                     1298 TGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCCACGAGA 1334
                                                                                                                                                                                                                         227 TGTCTGGAGGGAGTCCTTTCCTGCCAGCCCCAGGGA 263
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/organism="Rattus norvegicus"
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114 c 109 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 461.
Location/Qualifiers
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/lab_host="DH10B"
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Contact: Sleeman MA
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Jacks Breast, leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"

Alab host="E. coli EMDH108"

Anote="Vector: pcMYSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pglln.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pglln.pk008.c13 S' similar to gi|4506061 ref|NP 002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic gemma-1 [Homo sapiens] gi|12737489 ref|XP 006778.2| protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] BG113737489 ref|XP 006778.2| protein kinase, AMP-activated, gamma 1 non. mRNA sequence.
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/clone="pgmZn.pk005.j24"
/clone lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgmZn)"
/sex="Male and Female"
Gallus gallus
Waaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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1 (bases 1 to 636)
Burnaided, J., Morgan, R.W. and Cogburn, L.A.
Chicken ESTS from a normalized liver library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Breast muscle, leg muscle and epiphyseal growth plate"
                                                                                                    1 (bases 1 to 595)
Cogburn, L.A. and Monsonego-Ornan, E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project
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100.0%; Pred. No. 5.4;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Fax: Gogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/strain="Commercial broiler and
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AJ451523 rikenl Gallus gallus CDNA clone 29a6r1, mRNA sequence.
AJ451523
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1 (bases 1 to 687)

Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                         6 others
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Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 81-1345
Fax: 302-831-3411
Email: joan@UDel.Edu, www.chickest.udel.edu.
Location/Qualifiers
1. 636
/organism="Gallus_gailus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="riken1"
/cell_type="bursal lymphocyte"
/cell_type="bursal lymphocyte"
/note="CB inbred strain"
                                                                                                                                                 /db_xref="taxon:9031"
/clone="pgl1n.pk008.c13"
/clone_lib="Normalized Liver
/sex="Male and Female"
                                                                                                                                                                                                         /tissue type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
a 215 c 167 g 119 t
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/db_xref="taxon:9031"
/clone="29a6r1"
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RESULT 13 AJ396118

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AJ396118 AJ36118 dkfz426 Gallus gallus cDNA clone 25f16r1, mRNA sequence. AJ396118
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                          Gallus gallus
Vekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: WEL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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266320 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF601364
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/organism="Gallus gallus"

/strain="CB"

/db_xxef="texon:9031"

/clone="25fi6r1"

/clone lib="dkf2426"

/tissue_type="Bursa of Fabricius"

/cell_type="bursal lymphocyte"

/dev_stage="2-3 weeks old"

8 a 238 c 186 g 166 t
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100.0%; Pred. No. 5.8;
tive 0; Mismatches
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                                                                                                                                                             AJ396118.1 GI:7127728
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalla; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 124)

1 (bases I to 124)

1 (bases I to 124)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
v0.980904.e. Vector identified by cross_match with the -minscore 18
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PM2-ET0206-160101-001-f08 ET0206 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                     /db_xref="taxon:9913"
/tissue_type="pooled"
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/lab_host="0H108"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwigo.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-ET0206-160101-001-f08&t3=2001-01-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.4%; Score 23; DB 12; Length 474; Best Local Similarity 100.0%; Pred. No. 15; Matches 23; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone_lib="ET0206"
/dev_stage="Adult"
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                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 40 row: 0 column: 13
Seg primer: ATTTAGGTGACACTATAG.
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Email: asimpson@ludwig.org.br
                                                                                                                                                                   Location/Qualifiers
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                 and -minmatch 12 options.
PCR PRimers
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BI012981.1 GI:14417052
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VERSION
KEYWORDS
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MEDLINE
COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                FEATURES
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/note="Organ: lung_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of Lissue mRNA and cDNA amplification were performed under low stringency conditions."

ONIGIN

Query Match

1.3%; Score 22; DB 13; Length 124;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CV 1422 TCTCCTTCCGACATCCTTCA 1443

Db 107 TCTCCTCTCCGACATCCTTCA 86

Search completed: January 6, 2003, 11:08:01

Job time: 2115.51 secs
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breast cell foetal liver #13292 for g brain expres

Human AMPK gamma s Human AMPK gamma s AMP-activate

Human / Human Probe H Human D

genome-deriv

Title: Perfect score:

Sequence:

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nucleic

Run on:

Scoring table:

Minimum DB 8 Maximum DB 8

Database :

Nord size :

Searched:

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.
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ABS03407
AAH43685
AAD03296
AAD03320
ABA08485
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ABA67769
ABA34826
AAK16181
                                                                                           AAK41922
AAI22692
AAI47988
AAI08354
ABS15953
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AAD03319
AAD36456
AAD36457
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AAK17931
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/note= "3' portion of
14..95
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AAQ28398
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AAH43695
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AAC28698
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AAS46045
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612..736
/*tag= e
/number= "Intron 6"
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number= "Intron 5"
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  PRKAG3 intron 4 - intron 10.
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Human breast cell
Human foetal liver
Probe #3373 for ge
Human bone marrow
Probe #3389 for ge
Probe #3350 used t
Probe #3350 used t
                                                                                (without alignments)
11781.028 Million cell updates/sec
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| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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| SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn-embl
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                    2185239 seqs, 1125999159 residues
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                                                  nucleic search, using sw model
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ABA44706
ABA55162
ABA24907
AAK03423
AAK034821
AAI134621
AAI03344
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Gapop_60.0 , Gapext 60.0
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Score

Result

126459786

00000000

Human DNA encoding

Human bone marrow
Probe #12625 for g
Probe #12625 for g
Probe #16674 used
Probe #18167 used t
Human genome-deriv
Pig AMPK gamma sub
Pig AMPK gamma sub
Pig PRKAG3 polymor
Pig PRKAG3 gene c
Human ORFX polymuc
Human Coral liver
Human bone marrow
Probe #18511 used
Human bone marrow
Probe #18511 used
Human secreted pro
Membrane-bound pro

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180

360

360 420 420 480 480 540 540 009 009 099 999 720 720 780 780 840 840 900 900 960 960

300

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GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                             121 GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGAAAT
                                                                 ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTGCCATAGGTGCTAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution of P1AA; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCTATGGGACAGCAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG 120
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number= "Intron 7"
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number= "Intron 8"
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                                                                                                                                             "Exon
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                                                                                                                                                                                                         'number= "E
1689..1722
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                                                                        *tag= h
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                         CACCCTCATCAAGAACCGGATCCATCGCCTGCTGTTCTTGACCCGGTGTCAGGCAACGT
                                                 ACTCCACATCCTCACACACACACGCCTGCTCAAGTTCCTGCACATCTTTGTAAGCCTGGG
                                                                                                           CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA
                                                                                                                                                     TATCCAAGATTTGGGCATCGGCACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                          breast cell single exon nucleic acid probe #3401
                                                                                                                                                                                                        Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                              disease; cancer; ss
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contracting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label count to each probe of the microarray. The probes are useful for bound to each probe of the microarray of genomic DNA predicted to verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents afta greater captures for measuring gene expression, with far less bias than expressed sequence tam microarrays. The method is suitable for rapid production of functional information from genomic sequence. The propes are single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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          human
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useful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                             Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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100.0%; Pred. No. 1.6e-148;
iive 0; Mismatches 0;
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Matches 346; Conservative
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cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
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26-MAY-2000, 2000US-0207456.

30-JUN-2000, 2000US-0608408.

03-AUG-2000, 2000US-063366.

21-SEP-2000, 2000US-0234687.

27-SEP-2000, 2000US-0234687.

04-OCT-2000; 2000US-023459.
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                                                                                                               WO200157274-A2.
                                                                           Homo sapiens
                                                                                                                                                       09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human probe of the invention.

Probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTCTATGGGACAGCAAGAAGCAGGAGCTTTGTGGGTGAGGAGGAGGCTGAGGTGAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression; heart; microarray; vascular system; probe;
                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 378;
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 346; DB 22; L
Pred. No. 1.6e-148;
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100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                           Chen W, Rank DR
                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                     04-FEB-2000, 2000US-0180312.
26-MAY-2000, 2000US-0207456.
30-JUN-2000, 2000US-0608408.
03-AUG-2000, 2000US-0632366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0234687.
30-JAN-2001; 2001WO-US00669
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying sene expression in samples derived from the human heart via microarrays. By measuring sene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 346; DB 22; Length 378; 100.0%; Pred. No. 1.6e-148;
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20.1%; Score 340; DUBEST Local Similarity 100.0%; Pred. No. 1.6.
Matches 346; Conservative 0; Mismatches
                                                                                                                                                                                                   Claim 1; SEQ ID No 3373; 530pp; English.
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                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                           06-NOV-2001
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                                                                        AAK28874/c
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                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                  numen; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 CCCTCTATGGGACAGCAGAGAAGCAGGGCTTTCTGGGTGAGGAGGAGGGTGGGAGGTGGGAGGTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
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                                                                    Human brain expressed single exon probe SEQ ID NO: 3414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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                                                                                                                                                                                                                                                                                                                   Rank
                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                          03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                         2000US-0207456.
2000US-0608408.
          AAK03423 standard; DNA; 378
                                                                                                                                                                                          30-JAN-2001; 2001WO-US00667
                                                  (first entry)
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                                                                                                                                Homo sapiens
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30-JUN-2000;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful for ring gene expression in human bone marrow -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                           ATGACCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                               301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGC
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Pred. No. 1.6e-148;
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20.1%; Score 346; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 346; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                     BP.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488900/53
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                      Probe #3398 for gene expression analysis in human cervical cell sample.
                  300
                                                                                                                                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
181 ACCACAGGCTTCAGGCCAGGCCCAGGGGCCAGGGTGGAGAAAGTCCATCC
                                                                               GGAGTCTGCATGGCCAGCTGGGAAGACCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                            ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGC 346
                                                                                                                                           62 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.1%; Score 346; DB 22; I
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 3398; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000; 2000US-0180312.
26-MX-2000; 2000US-0207456.
30-UJN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                        RESULT 7
AA113465/c
ID AA113465 standard; DNA; 378
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                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer; ss
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                             Probe #3507 used to measure gene expression in human placenta sample.
CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGGAGGCTGGGGAAGGTGAAG
             GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
                                                                181 ACCACAAGCTTGGCTTCAGGCCAAGCCCAGGGGGCCAGGGTGGAGGAAAGTCCATCC
                                                                                                                 GGAGTCTGCATGGCCAGCTGGGAGCCCTGAGGCTCAATTTCCCCCATCTGTGGAGCCGCT
                                                                                                                                                                    GGAGTCTGCATGGCCAGCTGGAACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                             346
                                                                                                                                                                                                       Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0668408.
03-AUG-2000; 2000US-0621316.
21-SEP-2000; 2000US-0236359.
27-SEP-2000; 2000US-0236359.
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ID AAI34821 standard; DNA; 378
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Best Local Similarity 100.
Matches 346; Conservative
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ABS03407/c
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                                                                                                                        GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
                                                                                                    CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGGAGGTGAAG
                                                                                                                                                                                      GGAGATGGAGGAGGTGAGGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT
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                                                                                                                                                                                                                                                                                                                                                                                       CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCCATGGCCCTGTGC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID No 3335; 322pp; English.
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                              Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
breast cancer, disorders of development, inflammatory diseases
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                of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
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                                                                                                                                                                Query Match 20.1%; Score 346; DB 22; Length 378; Best Local Similarity 100.0%; Pred. No. 1.6e-148; Matches 346; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-234587P.
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WOLE-) MOLECULAR DYNAMICS INC.

Renn SG, Harzel DK, Chen W, Rank DR;

PS Spatially-addressable set of single exon nucleic acid probes, used to

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This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a C at nucleotide 550; and in exon 10
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                                                                                                                                                                                                                                                                                                                         WPI; 2001-657170/75.
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New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
182 ACCACAAAGCTTGGCTTCAGGCCAAGCCCAGGGCCAGGGCTGGAGGAAAGTCCATCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                         241 GGAGTCTGCATGGCCAGCTGGGAGCCCTGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
                                                                                                    122 GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGCTCAATTTCCCCATCTGTGGAGCCGCT
                                                                                                                                                                                      346
                                                                                                                                                                                                               62 ATGACCAGCTGACACCTTCACCTCCGCTACTGCATGGCCCTGTGC 17
                                                                                                                                                                       301 ATGACCAGCTGACACCTTTCACCTCCGCTACTGCATGGCCCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= "T559C"
/note= "Silent variation"
1037
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/label= "C1037T"
/note= "Causes R340W"
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/label= "C230G"
/note= "Causes P71A"
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/product= "PRKAG3"
                                                                                                                                                                                                                                                                                                                                                                             AAH43685 standard; cDNA; 1647 BP.
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WO200120003-A2
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                     myopathy
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                                                                                                                               GGTTCCCTGCTGCCCCGGCCCTTCCTTACCGCACTATCCAAGATTTGGGCATCGGC 1582
                                                                                                                                                                        ACATTCCGAGACTTGGCTGTGGTGCTGGAGACACCCATCCTGACTGCACTGGACATC 1642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine
monophosphate-activated kinase for diagnosis or treatment of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rogel-Gaillard C;
variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                                                                 Gaps
                                                                                                                                                                                             ACATTCCGAGACTTGGCTGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACTTCATC
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                                                                                                                                                                                                                                                                                                                                                           Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
                                                                                       DB 22; Length 1647;
                                                                                                                                                                                                                    TITGIGGACCGCCGGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1690
                                                                                                                                                                                                                               Indels
                                                               Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
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                                                                                           . 6e-67;
0;
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                                                                                      9.8%; Score 168; DB
100.0%; Pred. No. 6e-
ive 0; Mismatches
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ANDERSSON L.
LOOFT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                             AAD03296 standard; DNA; 2109 BP.
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472..1389
/*tag= b
/product= "F
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18-MAY-2000; 2000EP-0401388
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                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                               Best Local Similarity 100.
Matches 168; Conservative
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P-PSDB; AAE00221.
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(ANDE/) A
(LOOF/) 1
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The present sequence is a cDNA encoding human adenosine monophosphate

(AMP)-activated kinase (AMPK) gamma subunit muscle specific isoform,

PRKAG3. Mutation in Prkag3 results in an altered regulation of

PRKAG3. Mutation in Prkag3 results in an altered regulation of

carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular diseases, to modulate AMPK

activity, and for restoring a normal AMPK function. PRKAG3 sequence

and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect

a genetic polymorphic marker linked to a sequence encoding PRKAG3, are caseful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.

Transgenic animal and host cell transformed with PRKAG3 or a beterning compounds able to modulate AMPK activity, Nucleic acid

Compounds able to modulate AMPK activity, Nucleic acid

Compounds able to modulate AMPK activity, Nucleic acid
                                                                                                                                                                                                                                                                      Buch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1523 GGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1583 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATC 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
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associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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/product= "Human complete Prkag3 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 168; DB 22;
100.0%; Pred. No. 5.9e-67;
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Conservative 0; Mismatches
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1..1395
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                                                                                  Claim 12; Fig 2; 71pp; English
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Matches 168; Conserv
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The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutration in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism, particularly in skeletal muscle metabolism so diabetes, obesity, and disorders associated with muscle metabolism cuch as myopathy and cardiovascular diseases, to modulate AMPK cortivity, and for restoring a normal AMPK function. PRKAG3 sequence are into a genetic testing and prognosis of a metabolic disorder. C and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder. C a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3, are useful for detecting campounds able to modulate AMPK activity. Nucleic acid correcting compounds able to modulate AMPK activity. Nucleic acid secenting compounds able to modulate AMPK activity. Nucleic acid in a sequence encoding PRKAG3 in a sequence encoding the first cystathione beta synthase (CBS) domain
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haematopoiesis regulation, tissue growth, immunomodulator, activin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                 Robic A, Rogel-Gaillard C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1583 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATC 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928 GGTTCCCTGCTGCCCGGCCCTCCTTCCTCTACCGCACTATCCAGATTTGGGCATCGGC 987
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Pred. No. 5.9e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
                                                                                                               Looft C, Kalm E, Milan D, Robic Gellin J, Le Roy P, Chardon P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No.
                                      (INRG ) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.
                                                                                                                                                                                                                                                                  Claim 12; Page 65-68; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA08485 standard; cDNA; 547 BP.
 10-SEP-1999; 99EP-0402236.
18-MAY-2000; 2000EP-0401388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.84;
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                                                                                                                                                     WPI; 2001-244810/25.
P-PSDB; AAE00223.
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                                                                                                                           Iannuccelli N,
                                                                                  KALM E.
                                                                                                               Andersson L,
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proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid dell disorder; hymbhold cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiarthritic; haemostatic; antiarthritic; haemostatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasouropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
inhibin; chemotaxis; chemokinesis; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT;
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27-APR-2000; 2000US-0560875.
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P-PSDB; ABB11241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157188-A2.
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 1; Page 429; 1963pp; English.

control also relates to vectors and recombinant host competities, and substitues ABAR08225-ABAR09274 represent mucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and methods of producing the novel polypeptides of the invention. Although novel, many of the collypeptides for the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention may differential therapeutic applications activities; and hence contactic or chemokinetic activities; haematopolical activities; chemotactic or chemokinetic activities; haematopolical activities; contactic or chemokinetic activities; haematopolical activities; contactic or chemokinetic activities; pacestation or metastasis. Chemotactic or chemokinetic activities; propheptides and nucleotides of the invention are useful for preventing. Treating or ameliorating medical contactic or chemokinetic activities polypeptides and nucleotides of the invention are useful for preventing. Treating or aneliorating cancer cancers, haematopoletic disorders (e.g., may be used to promit disorders), conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., ostoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and fungal infections in addition to immune disorders (e.g., ostoporosis), while those with immunomodulatory activities may be used in the treatment of viral, menniquate encell growth factor activity may be used to neucoperterial and fungal infections in addition to immune disorders (e.g., propheptides that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention. Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides,

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                                                                  1523 GGTTCCCTGCTGCCCCGGCCCTCCTTCCTACCGCACTATCCAAGATTTGGGCATCGGC 1582
                                                                                                                1583 ACATTCCGAGACTTGGCTGTGGTGCTGGAGACAGCACCCATCCTGACTGCACTGGACATC 1642
                                                                                                                              285 GGTTCCCTGCTGCCCCGGCCCTCCTTCCTCTACCGCACTATCCAAGATTTGGGCATCGGC 344
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast;
                         Length 547;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                Human breast cell single exon nucleic acid probe #8545.
Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
                       Query Match
8.5%; Score 147; DB 22;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 147; Conservative 0; Mismatches 0;
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                                                                                                                                                              TTTGTGGACCGGCGTGTGTCTGCACTG 1669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                            ABA49850 standard; DNA; 92
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                    disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                WO200157271-A2.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for spending breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on calls. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias

Claim 4; SEQ ID NO 8545; 327pp + sequence listing; English.

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than expressed sequence tag microarrays. The method is suitable for
                            rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                  1 CCTGGCCCCTCAGATCAAGAAGGCCTTCTTTGCTCTGGTGGCCAACGGTGTGCGGCAGC 60
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100.0%; Pred. No. 1.3e-19;
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He : 336.168 secs
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